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(57) Abstract

A method of modulating the ripening and/or senescence characteristics in plants of the genus *Musa* comprises transforming plants with one or more sequences obtainable from the deposited cDNA library having the accession number 40184, regenerating said plants and selecting from the population of transformants those plants having modulated and/or tissue senescence characteristics.

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GENETIC CONTROL OF FRUIT RIPENING

This invention relates generally to the modification of a plant phenotype by the regulation of plant gene expression. More specifically it relates to the modulation of the ripening and/or tissue senescence characteristics and plants derived therefrom. One suitable application of the present invention is the modulation of ripening and/or senescence processes in plants of the genus *Musa* (referred to herein as banana).

Two principal methods for the control of expression are known, viz.: overexpression and underexpression. Overexpression may be achieved by insertion of one or more than one extra copies of the selected gene. It is, however, not unknown for plants or their progeny, originally transformed with one or more than one extra copy of a nucleotide sequence, to exhibit the effects of underexpression as well as overexpression.

For underexpression, often referred to as "gene silencing", there are two principle methods which are commonly referred to in the art as "antisense downregulation" and "sense downregulation (also referred to as "cosuppression"). Both of these methods lead to an inhibition of expression of the target gene. Other lesser used methods involve modification of the genetic control elements, the promoter and control sequences, to achieve greater or lesser expression of an inserted gene.

There is no reason to doubt the operability of these methods: they are well- established, used routinely in laboratories around the world and products in which they have been used are on the market.

Gene control by any of these methods requires the insertion of a selected gene or genes into plant material which can be regenerated into plants. This transformation process can be performed via a number of methods, for example: the *Agrobacterium*-mediated transformation method.

In the microparticle bombardment method, microparticles of dense material, usually gold or tungsten, are fired at high velocity at the target cells where they penetrate the cells, opening an aperture in the cell wall through which DNA may enter. The DNA may be coated on to the microparticles or may be added to the culture medium.

In microinjection, the DNA is inserted by injection into individual cells via an ultrafine hollow needle.

Another method, viz. fibre-mediated transformation, applicable to both monocots and dicots, involves creating a suspension of the target cells in a liquid, adding microscopic needle-like material, such as silicon carbide or silicon nitride "whiskers", and agitating so that the cells and whiskers collide and DNA present in the liquid enters the cell.

In summary, then, the requirements for both sense and antisense technology are known and the methods by which the required sequences may be introduced are known. What remains, then is to identify genes whose regulation will be expected to have a desired effect, isolate them or isolate a fragment of sufficiently effective length, construct a chimeric gene in which the effective fragment is inserted between promoter and termination signals, and insert the construct into cells of the target plant species by transformation. Whole plants may then be regenerated from the transformed cells.

Bananas are a globally important fruit crop. They are not only a popular dessert fruit, but represent a vital carbohydrate staple in the tropics with as many as 100 million people subsisting on bananas and plantains as their main energy source. The cultivated dessert banana is commonly triploid, parthenocarpic and belongs to the *Musa* AAA genome group, eg. Cavendish subtypes. Bananas are climacteric fruits and ripening is regulated by ethylene produced by the fruit and involves numerous biochemical changes including the conversion of starch to sugars, cell wall disassembly, synthesis of volatile compounds, changes in phenolic constituents and degradation of chlorophyll in the peel. The conversion of starch to sugars is particularly striking, where starch accounts for 20-25% of the fresh weight of the unripe fruit and depending on the genetic background, can be converted almost entirely to sugars.

The triploid nature of the cultivated dessert banana crop has hampered conventional methods of breeding for improved characteristics. As a result of this an enormous pool of genetic resources for enhancing postharvest characteristics of the fruit has remained untapped.

According to the present invention there is provided a method of modulating the ripening or tissue senescence process in plants of the genus *Musa* comprising inserting into plant material at least one polynucleotide sequence selected from the sequences depicted as SEQ ID-Nos. 1 -57, regenerating said plant material and selecting from the transformed

regenerants, plants with modulated ripening or tissue senescence characteristics. The said polynucleotide may be obtained from the cDNA library having the NCIMB Accession Number 40814.

Further according to the present invention is a method of modulating the ripening or tissue senescence process in plants of the genus *Musa* comprising inserting into plant material at least one polynucleotide sequence or a fragment thereof, obtainable by hybridisation, from the cDNA library having the NCIMB Accession Number 40814, by the use of at least one of the sequences depicted as SEQ ID Nos 1-57 as oligonucleotide probes, said hybridisation being conducted at a temperature from 60°C to 65°C in 0.3 strength citrate buffered saline containing 0.1% SDS followed by rinsing at the same temperature with 0.3 strength citrate buffered saline containing 0.1% SDS, regenerating said plant material and selecting from the transformed regenerants, plants with modulated ripening or tissue senescence characteristics. The invention further provides a method as described above wherein the said polynucleotide is capable of modulating the production of pectate lyase and more specifically the polynucleotide comprises at least one of the sequences depicted in the sequence listings as SEQ-ID-Nos. 13-18.

A preferred method for inserting the said polynucleotides into plant material according to the method of the present invention, may be selected from the group comprising the *Agrobacterium*, microparticle bombardment, fibre mediated or direct insertion methods.

The invention further provides plants, their progeny and seed and material obtained from said plants, produced according to the method of the present invention. It is preferred that the said plants, their progeny and seed and material obtained from said plants are derived from plants of the genus *Musa*.

The present invention also provides a vector functional in plants comprising a promoter region which is operable in plant cells, at least one of the polynucleotide sequences described above and a transcription termination sequence. The promoter may be constitutive, developmentally regulated or switchable. In addition to this the promoter may also be tissue specific or organ specific.

Further provided is a banana produced via the preceding method, having altered fruit characteristics when compared with a banana which is not transformed with at least one of the polynucleotide sequences described above.

The present invention also provides an improved method of controlling plant pathogens comprising the application of an anti-pathogenic agent to plants, characterised in that plants to which the said agent is applied, are plants according to the present invention.

The gene sequences of the present invention may be synthesised *ab initio*, using the sequence data in the sequence listing provided herewith, or isolated from a library using the standard techniques know within the art. The sequences depicted in the sequence listing or parts thereof may also be used to create oligonucleotide probes for the purposes of isolating from the library those polynucleotides which are capable of producing the desired proteins. To assist the isolation of these polynucleotides we have deposited with the National Collection of Industrial & Marine Bacteria, St. Machar Drive, Aberdeen, UK, a cDNA library of the banana peel ripening related genes. The library was deposited on 9th July 1996 and has the NCIMB Accession Number 40814.

Thus, this invention is based on the identification of genes which encode proteins involved in banana ripening-related processes, specifically within banana pulp. DNA sequences according to the sequence listing or those sequences obtainable from the deposited library, may be used in the process of modifying the plant ripening characteristics of plants and/or fruit.

By virtue of this invention banana plants can be generated which, amongst other phenotypic modifications, may have one or more of the following fruit characteristics: improved resistance to damage during harvest, packaging and transportation due to slowing of the ripening and over-ripening processes; longer shelf life and better storage characteristics due to reduced activity of degradative pathways (e.g. cell wall hydrolysis); improved processing characteristics due to changed activity of proteins/enzymes contributing to factors such as: viscosity, solids, pH, elasticity; improved flavour and aroma at the point of sale due to modification of the sugar/acid balance and other flavour and aroma components responsible for characteristics of the ripe fruit; modified colour due to changes in activity of enzymes involved in the pathways of pigment biosynthesis (e.g. lycopene, β-carotene, chalcones and anthocyanins); increased resistance to post-harvest pathogens such as fungi.

The activity of the ripening-related proteins may be either increased or reduced depending on the characteristics desired for the modified plant part (fruit, leaf, flower, etc). The levels of protein may be increased: for example, by incorporation of additional genes. The additional

genes may be designed to give either the same or different spatial and temporal patterns of expression in the fruit. "Antisense" or "partial sense" or other techniques may be used to reduce the expression of ripening-related protein.

The activity of each ripening-related protein or enzyme may be modified either individually or in combination with modification of the activity of one or more other ripening- related proteins/enzymes. In addition, the activities of the ripening-related proteins/enzymes may be modified in combination with modification of the activity of other enzymes involved in fruit ripening or related processes.

DNA constructs according to the invention for gene silencing, may comprise a base sequence at least 10 bases (preferably at least 35 bases) in length for transcription into RNA. There is no theoretical upper limit to the base sequence, it may be as long as the relevant mRNA produced by the cell but for convenience it will generally be found suitable to use sequences between 100 and 1000 bases in length. When using genomic DNA as the source of a base sequence for transcription it is possible to use either intron or exon regions or a combination of both.

As a source of the DNA base sequence for transcription, a suitable cDNA or genomic DNA or synthetic polynucleotide may be used. The isolation of suitable ripening-related sequences is described above; it is convenient to use DNA sequences derived from the ripening-related clones deposited at NCIMB in Aberdeen. Sequences coding for the whole. or substantially the whole, of the appropriate ripening-related protein may thus be obtained. Suitable lengths of this DNA sequence may be cut out for use by means of restriction enzymes. The preparation of such constructs is described in more detail below.

Constructs suitable for expression of the appropriate ripening-related sequence in banana cells, may be produced using a cDNA sequence selected from the deposited library having the NCIMB Accession Number 40814 or the gene sequence as found in the chromosome of the banana plant. Recombinant DNA constructs may be made using standard techniques.

In this specification modulation means an increase or decrease of the desired effect. More specifically "modulation of the ripening or tissue senescence process in plants of the genus *Musa*" means an increase or decrease in production of a ripening related protein resulting from the method as described above. For example, where an increased ripening related protein is desired. plants may be transformed according to the method as described

above and those plants exhibiting the desired effect may be selected from the population of transformants. Furthermore, it may be desirable to provide a plant with modulated ripening or tissue senescence characteristics by increasing the production of one protein and decreasing the production of another protein in the same plant. For example, a banana fruit, modified using the present method, and having decreased levels of the enzyme pectate lyase would be beneficial because pulp softening would require a substantially longer time when compared with a control. In addition to this and by increasing the levels of another ripening related protein such as an antifungal protein in the same fruit using the present method, would complement the extended life of the banana pulp with increased resistance to disease.

Increase in production of a ripening related protein includes inserting into plant material one or more copies of any of the polynucleotides described above, wherein the said polynucleotides must be capable of producing a protein and thereby increasing protein levels when compared with a control plant.

Decrease in production of a ripening related protein includes inserting into plant material one or more copies of any of the polynucleotides described above, wherein the said polynucleotides must be capable of producing an mRNA which is capable of interfering with endogenous mRNA to such a degree that the levels of translated protein are reduced when compared with a control plant.

Ripening process of plants means the process of maturing or developing .

Senescence means the progressive deterioration in function of cells, tissues, organs etc., related to the period of time since that function commenced..

Control plant means a comparable plant used for the purposes of determining modulation of the ripening or tissue senescence process effect in plants. Specifically, in plant transformations the control plant is usually of the same species and variety as the material used before the transformation process and is grown in the same conditions, (usually with the transformant selection step modified in some way on the part of the control plant), as the transformed plants. More specifically the control plant may comprise an untransformed control plant or a transformed control plant providing it has not already been transformed with the same polynucleotide sequence as the plant material to be transformed.

"Plant material" includes plant cells and any other type of plant regenerable material.

The following examples further illustrate the invention but are not to be construed to limit the scope thereof:

TABLE 1. Is a list of clones isolated from banana pulp and the corresponding sequence identity number as provided in the sequence listing herein. The table also illustrates the approximate clone size, the percentage identity and, where relevant, nucleotide similarity with published sequences, based on the results obtained from comparisons with the EMBL sequence database. The table also provides, where relevant, the gene identity of those published sequences and their database accession numbers.

FIGURE 1. Plant transformation vector pUN, containing the UBI polyubiquitin promoter.

FIGURE 2. Plant transformation vector pSHYN, containing hygromycin resistance gene for selection of transformed plants.

FIGURE 3. Plant transformation vector pAN, containing the banana ACC oxidase promoter.

EXAMPLE 1

Construction of a cDNA library of ripening genes

1.1 Isolation of messenger RNA

Total RNA was isolated from ripening (24 hours after ethylene treatment) banana pulp (*Musa acuminata* cv. Grand Nain) as described by Chang et al, Plant Molecular Biology Reporter, Vol. 11(2) 113-116 (1993). Messenger RNA was isolated from total RNA by Oligo(dT)-cellulose chromatography according to Bantle et al., Analytical Biochemistry 72, 413-427 (1976).

1.2 Synthesis of cDNA and Cloning into Vector

The first and second strands of the cDNAs were synthesised from the messenger RNAs using a commercial cDNA synthesis kit (Catalog No. 200450, ZAP Express™ Gold Cloning kit, Stratagene Ltd, Cambridge, Cambs, UK). Double stranded cDNAs were cloned into the ZAP Express™ vector, packaged, mixed with plating bacteria to determine titre and for library screening, following instructions of the suppliers protocol.

1.3 Screening of the cDNA library from banana pulp.

The unamplified cDNA library from ripening banana pulp was differentially screened using cDNA from unripe and ripening banana peel tissue. A proportion of the library was plated individually at low density and duplicate plaque lifts made onto Hybond N nylon filters (Amersham) according to the manufacturer's instructions. One filter was hybridised to dCTP radiolabelled cDNA from green fruit and the duplicate filter hybridised to dCTP radiolabelled cDNA from ripening fruit. Hybridization's were at high stringency. Plaques hybridising preferentially with ripening or green radiolabelled cDNA were picked and re-plated for a second round of selection by differential screening. These clones were numbered as ripening up- or down-regulated peel clones. The clones were in-vivo excised from the ZAP express™ vector into the pBK-CMV phagemid vector using the ExAssist™ interference-resistant helper phage, following instructions from manufacturers protocol.

1.4 Characterisation of the ripening pulp cDNA library and the ripening-related clones.

The ripening cDNA library from pulp tissue were prepared with an efficiency of 3.2×10^5 plaque-forming units per microgram of cDNA. The sizes of the inserts in the peel library was 0.4 - 6.7 Kb with a mean size insert of 1.47 Kb.

From the 250 plaques used in the first screen, 73 putative ripening-related clones were obtained. These 73 clones were partially sequenced using the ABI PRISMTM Dye Terminator Cycle Sequencing Ready Reaction kit with AmpliTaq® DNA polymerise (Applied Biosystems, Warrington, Cheshire, UK) with forward primers specific for the pBK-CMV vector. From these, the following ripening-related clones were selected. Comparisons of these sequences in the EMBL database using GCG ('Wisconsing') software has identified homologies for the clones listed in TABLE 1 below.

EXAMPLE 2

Construction of truncated sense RNA vectors with the maize polyubiquitin promoter.

A vector is constructed using the sequences corresponding to a fragment of the inserts of one of the sequences 1 to 57. This fragment is synthesised by polymerase chain reaction using synthetic primers incorporating BamHI restriction sites suitable for cloning between a

maize UBI polyubiquitin promoter (Christensen et al, 1992, Plant Molecular Biology, 18:675-689) and a nopaline synthase 3'end termination sequences in the vector pUN (Fig. 1.).

The truncated sense expression cassette is excised by digestion with AscI, the ends of the fragment are made flush with T4 polymerase and it is cloned into the vector pSHYN (Fig. 2.) which has been cut with KpnI and the ends made flush with Klenow polymerase. pSHYN contains hygromycin resistance gene for selection of transformed plants.

After synthesis of the vector, the structure and orientation of the sequences are confirmed by DNA sequence analysis.

EXAMPLE 3

Construction of truncated sense RNA vectors with a fruit enhanced promoter.

The 1386bp HindIII fragment containing the banana ACC oxidase promoter (UK. Application No. 9607700.3) is cloned the HindIII site in pMSC2 (Fig. 3.) to give the vector pAN.

A vector is constructed using the sequences corresponding to a fragment of the inserts of one of the sequences 1 to 57. This fragment is synthesised by polymerase chain reaction using synthetic primers incorporating BamHI restriction sites suitable for cloning between a maize UBI polyubiquitin promoter (Christensen et al, 1992, Plant Molecular Biology, 18:675-689) and a nopaline synthase 3'end termination sequences in the vector pAN.

The truncated sense expression cassette is excised by digestion with AscI, the ends of the fragment are made flush with T4 polymerase and it is cloned into the vector pSHYN (Fig. 2.) which has been cut with KpnI and the ends made flush with Klenow polymerase. pSHYN contains hygromycin resistance gene for selection of transformed plants.

After synthesis of the vector, the structure and orientation of the sequences are confirmed by DNA sequence analysis.

EXAMPLE 4

Construction of an over-expression vector with the maize polyubiquitin promoter.

The complete sequence of a ripening -related cDNA containing a full open-reading frame is inserted into the vectors described in EXAMPLE 2.

EXAMPLE 5

Construction of an over-expression vector with a fruit enhanced promoter.

The complete sequence of a ripening -related cDNA containing a full open-reading frame is inserted into the vectors described in EXAMPLE 3.

EXAMPLE 6

Generation of transformed Musa plants

Transformed Musa plants containing the vectors are produced by the method described in Sagi et al. (1995) Biotechnology. Vol. 13 pp 481-485. Regenerated transformed plants are identified by their ability to grow on hygromycin and grown to maturity. Ripening fruit are analysed for a modulation in their ripening related or senescence characteristics.

Other suitable transformation methods for banana are described in Sagi et al. (1994) Plant Cell Reports. Vol. 13. pp 262-266. and May et al. (1995) Biotechnology. Vol. 13 pp 486-492.

TABLE 1

Sequence Identity	Group	Clone no.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ-ID-NO-1	Pulp Upregulated	U-U9	1	Isoflavone Reductase	61.6	714	Potato (*Solanum tuberosum*), X92075
SEQ-ID-NO-2	Pulp Upregulated	U-U17	1	Isoflavone Reductase	62.9	770	Potato (*Solanum tuberosum*), X92075
SEQ-ID-NO-3	Pulp Upregulated	U-U66	1.1	Isoflavonoid Reductase	60.0	722	*Arabidopsis thailiana*, Z49777
SEQ-ID-NO-4	Pulp Upregulated	U-U104	1	Isoflavonoid Reductase	60.6	696	*Arabidopsis thailiana* Z49777
SEQ -ID-NO-5	Pulp Upregulated	U-U13	1.1	Beta-1,3-Glucanase	58.5	585	Soybean (*Glycine max*), A26451
SEQ -ID-NO-6	Pulp Upregulated	U-U136	1.3	Beta-1,3-Glucanase	59.8	800	Barley (*Hordeum vulgare*), M91814
SEQ -ID-NO-7	Pulp Upregulated	U-U21	1.8	Transcriptional Activator	54.3	311	*Zea mays*, L13454

Sequence Identity	Group	Clone no.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ -ID-NO-8	Pulp Upregulated	U-U31	0.55	S-adenosylhomocysteine Hydrolase	67.0	467	Orchid (*Phalaenopsis sp.*), X79905
SEQ -ID-NO-9	Pulp Upregulated	U-U131	1.8	S-adenosyl L-homocysteine Hydrolase	79.8	699	Wheat (*Triticum aestivum*), L11872
SEQ -ID-NO-10	Pulp Upregulated	U-U32	0.8	Beta-amylase	54.7	854	*Zea mays*, Z25871
SEQ -ID-NO-11	Pulp Upregulated	U-U55	0.8	O-methyl transferases	60.1	223	*Zea mays*, L14063
SEQ -ID-NO-12	Pulp Upregulated	U-U72	0.8	O-methyl transferase	60.6	226	*Zea mays*, L14063
SEQ -ID-NO-13	Pulp Upregulated	U-U68	1.8	Pectate Lyase	57.9	394	*Lilium longiflorum*, Z17328
SEQ -ID-NO-14	Pulp Upregulated	U-U69	1.7	Pectate Lyase	66.1	516	*Zea mays*, L20140
SEQ -ID-NO-15	Pulp Upregulated	U-U84	1.1	Pectate Lyase	65.8	736	*Lycopersicon esculentum*, X55193
SEQ -ID-NO-16	Pulp Upregulated	U-U89	1.6	Pectate Lyase	54.8	354	*Nicotiana tabacum*, X67158

Sequence Identity	Group	Clone no.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ -ID-NO-17	Pulp Upregulated	U-U115	1.5	Pectate Lyase	67.3	508	*Zea mays*, L20140
SEQ -ID-NO-18	Pulp Upregulated	U-U117	1.7	Pectate Lyase	55.0	333	*Lilium longiflorum*, Z17328
SEQ -ID-NO-19	Pulp Upregulated	U-U80	0.6	Vicilin-like storage protein	53.7	387	*Arabidopsis thailiana*, T13642
SEQ -ID-NO-20	Pulp Upregulated	U-U90	1.8	Glutamate Descarboxylase	72.5	735	*Petunia hybrida*, L16797
SEQ -ID-NO-21	Pulp Upregulated	U-U92	1.8	Glutamate Descarboxylase	71.8	740	*Arabidopsis thailiana*, U10034
SEQ -ID-NO-22	Pulp Upregulated	U-U91	1.1	Aconitase	76.4	766	Pumpkin (*Cucurbita sp.*), D29629
SEQ -ID-NO-23	Pulp Upregulated	U-U96	0.9	Express Sequence Tag.	69.0	452	*Arabidopsis thailiana*, H36910
SEQ -ID-NO-24	Pulp Upregulated	U-U103	2	Cell Wall Invertase	66.0	567	*Zea mays*, U17695
SEQ -ID-NO-25	Pulp Upregulated	U-U93	3.5	Heat Shock Protein cognate	76.4	711	*Lycopersicon esculentum*, X54030
SEQ -ID-NO-26	Pulp Upregulated	U-U125	1.8	Heat Shock Protein	71.0	662	*Spinacia oleracea*, L26243
SEQ -ID-NO-27	Pulp Upregulated	U-U105	0.9	Hexaubiquitin Protein	64.1	237	Sunflower (*Helianthus annuus*), X57004

Sequence Identity	Group	Clone no.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ -ID-NO-28	Pulp Upregulated	U-U116	0.8	Polyubiquitin	81.0	625	Rice (*Oryza sativa*), X76064
SEQ -ID-NO-29	Pulp Upregulated	U-U120	0.9	Extensin	56.9	576	Almond (*Prunus amygdalus*), X65718
SEQ -ID-NO-30	Pulp Upregulated	U-U126	1.2	Basic Chitinase	63.2	506	Cowpea (*Vigna unguiculata*), X88801
SEQ -ID-NO-31	Pulp Upregulated	U-U129	1.3	Beta-glucosidase	60.9	517	White clover (*Trifolium repens*), X56733
SEQ -ID-NO-32	Pulp Upregulated	U-U130	1.3	Chlorophyll a/b binding protein	52.0	415	Rice (*Oryza sativa*), D00641
SEQ -ID-NO-33	Pulp Upregulated	U-U43	2.5	Fruit sp pp involved in maturation	53.8	396	Tomato (*Lycopersicon esculentum*), X13743
SEQ -ID-NO-34	Pulp Upregulated	U-U70	0.6	Root specific protein	63.6	420	Rice (*Oryza sativa*), L27208
SEQ -ID-NO-35	Pulp Upregulated	U-U16	0.6	-	-	-	No published sequence similarity
SEQ -ID-NO-36	Pulp Upregulated	U-U30	0.8	-	-	-	-
SEQ -ID-NO-37	Pulp Upregulated	U-U40	10	-	-	-	-
SEQ -ID-NO-38	Pulp Upregulated	U-U108	1.1	-	-	-	-

Sequence Identity	Group	Clone no.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ -ID-NO-39	Pulp Upregulated	U-U128	2.2	-	-	-	-
SEQ -ID-NO-40	Pulp Down regulated	U-D4	1.3	Granule Bond Starch Synthase	62.3	621	Cassava (*Manihot esculenta*), X74160
SEQ -ID-NO-41	Pulp Down regulated	U-D10	1.3	Starch Synthase	68.8	506	Pea (*Pisum sativum*), X88789
SEQ -ID-NO-42	Pulp Down regulated	U-D13	1.3	Starch Synthase	67.4	454	Pea (*Pisum sativum*), X88789
SEQ -ID-NO-43	Pulp Down regulated	U-D66	1.3	Granule Bond Starch Synthase	64.1	669	Cassava (*Manihot esculenta*), X74160
SEQ -ID-NO-44	Pulp Down regulated	U-D111	1.3	Starch Synthase	66.4	655	Cassava (*Manihot esculenta*), X74160
SEQ -ID-NO-45	Pulp Down regulated	U-D112	2.3	Granule Bond Starch Synthase	68.4	196	Potato (*Solanum tuberosum*), X58453

Sequence Identity	Group	Clone no.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ -ID-NO-46	Pulp Down regulated	U-D39	1.1	Antifungal Protein	69.1	517	*Zea mays*, U06831
SEQ -ID-NO-47	Pulp Down regulated	U-D50	1.3	Basic Chitinase	60.2	678	Cowpea (*Vigna unguiculata*), X88801
SEQ -ID-NO-48	Pulp Down regulated	U-D86	1.7	Basic Chitinase	63	578	Cowpea (*Vigna unguiculata*), X88801
SEQ -ID-NO-49	Pulp Down regulated	U-D90	1.3	Basic Chitinase	61.8	670	Cowpea (*Vigna unguiculata*), X88801
SEQ -ID-NO-50	Pulp Down regulated	U-D93	0.7	Basic Chitinase	61.6	701	Cowpea (*Vigna unguiculata*), X88801
SEQ -ID-NO-51	Pulp Down regulated	U-D61	1	Beta-glucanase	61.9	795	Barley (*Hordeum vulgare*), X52572
SEQ -ID-NO-52	Pulp Down regulated	U-D63	2.3	Nodulin Gene	50.4	637	Luceme (*Medicago sativa*), X13287

Sequence Identity	Group	Clone no.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ -ID-NO-53	Pulp Down regulated	U-D65	0.9	Extensin	56.7	556	Cowpea (*Vigna unguiculata*), X91836
SEQ -ID-NO-54	Pulp Down regulated	U-D84	0.8	Extensin	58.3	492	Cowpea (*Vigna unguiculata*), X91836
SEQ -ID-NO-55	Pulp Down regulated	U-D75	1.2	Wali 7	74.4	703	Wheat (*Triticum aestivum*), L28008
SEQ -ID-NO-56	Pulp Down regulated	U-D83	1.2	Wali 7	72.8	743	Wheat (*Triticum aestivum*), L28008
SEQ -ID-NO-57	Pulp Down regulated	U-D64	2.3	-	-	-	-

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: ZENECA LIMITED
(B) STREET: 15 STANHOPE GATE
(C) CITY: LONDON
(D) STATE: LONDON
(E) COUNTRY: UNITED KINGDOM
(F) POSTAL CODE (ZIP): W1Y 6LN

(ii) TITLE OF INVENTION: GENETIC CONTROL OF FRUIT RIPENING

(iii) NUMBER OF SEQUENCES: 57

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:
APPLICATION NUMBER: GB PPD

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 785 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGGCACGAGG AAAAACTANG TGAGAANGAG ATAATCGTTG ACCGAGGNAG AGAATGGCGA 60

GCGAGAAGAG CAAAATCCTG ATCATCGGGG GCACCGGGTA CATCGGCAAG TTCATCGTGT 120

TTGCGAGCGC CAGGTTAGGT AACCCTACCT TCGCTCTCGT CCGGAGCACC ACCGCCCCCG 180

CCGGCCAACC CGAGAAGGCC AAGCTCCTGA GCGACTTCCA GGCCGCCGGC GTCACCCTCG 240

TCCAGGGGGA TATNTATAAC CACGAGAGTC TGGTTAAGGC GATCAAGCTG GTGGATGTGG 300

TCATCTCCCC CGTCGGCTTC GGGCANCTGA NTGATCAGAC CAAGATCATC GACGCCATCN 360

AANAAGCCGG AGGACACATC AAGAGGTACC TTCCATCGGA GTTTGGCAAC GACGTANACC 420

GAAGCCATGC TGTGGAGCCA GCAAAGTCTA CCTTTGTCGT CAAGCAACAA ATCANAAGGG 480

CTGTTGAGGC ATCGGGTNTC CCTTACACCT TTGTATCTTC CAACTTTCTT CGGTGGGTNT 540

TTCCTCCCGG TATTATGACA GGCAGGAGCC ACTGGTCCTC CCACGGACAA GGTTGTCATC 600

TTAGGTNACG GGAACNCAAA ACGATCTTCT CNATGAANAC GACTTCCGGA CATCCCATTT 660

ANTCTTGGAT GATCCATAAC CTGAACCAGG TTCTATTTCT TAAAACTTCC NCCACTTCTT 720

NTCTCTTANC ANCTCNTTTC CCTCTTGGGA AAAAAATGTC NNCTANACTT CNAAAAGGGT 780

TTANT 785

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 813 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CGCGCACGAG GAAGAAAACT AGGTGAGAAN GAGATAATCG TTGACCGAGG NAGAGAATGG 60

CGAGCGAGAA GAGCAAAATC CTGATCATCG GGGGCACCGG GTACATCGGC AAGTTCATCG 120

TGTTTGCGAG CGCCAGGTTA GGTAACCCTA CCTTCGCTCT CGTCCGGAGC ACCACCGCCC 180

CCGCCGGCCA ACCCGAGAAG GCCAAGCTCC TGAGCGACTT CCAGGCCGCC GGCGTCACCC 240

TCGTCCAGGG GGATATATAT AACCACGAGA GTCTGGTTAA GGCGATCAAG CTGGTGGATG 300

TGGTCATCTC CCCCGTCGGC TTCGGGCANC TGANTGATCA GACCAAGATC ATCGACGCCA 360

TCAAAGAAGC CGGAGGACAC ATCAAGAGGT ACCTTCCATC GGAGTTTGGC AACGACGTAN 420

ACCGAAGCCA TGCTGTGGAG CCAGCAAAGT CGACCTTTGT CGTCAAGCAA CAAATCANAA 480

GGGCTGTTGA GGCATCGGGT ATCCCTTACA CCTTTGTATC TTCCAACTTC TTCGGTGGGT 540

NTTTCCTCCC GGTATTANGA CAGGCAGGAG CCACTGGTCC TCCCACGGAC AAGGTTGTCA 600

TCTTANGTGA CGGGAACACA AAAGCGATCT TTCTCAATGA ANACACATCC GGACNTNCAC 660

NATTAAAGCA GTGGATGATC CGAAAACCTG AACANGTTCT ATATCTGAAA CCTTCCGCCA 720

CTCTTGTCTC ATNACAACTC ATTTCCCTCT GGGAAAAAAA NGTCNGCAAA ACTCCNAAAA 780

GGTCTACTTC CCGGAAGAAA AATCTGAANC ANA 813

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 746 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGCACGAGGG GAAAAGGAGA TNATCGTTGA CCGAGGAGAG AATGGCGAGC GAGAAGAGCA 60

AGATCCTGAT CATCGGGGGC ACGGGGTACA TCGGCAAGTT CATCGTGTTT GCGAGCGCCA 120

GGTTAGGTAA CCCTACCTTC GCTCTCGTCC GGAGCACCAC CGCCCCCGCC GGCCAACCCG 180

AGAAGGGCAA GCTCCTGAGC GACTTCCAGG CCGCCGGCGT CACCCTGGTC CAGGGGGATA 240

TATATAACCA CNAGAGTCTG GTTAAGGCGA TCAAGCTGGT GGATGTGGTC ATCTCCCCCG 300

TCGGCTTCGG GCAGCTGAGT GATCAGACTA AGATCATCGA CGCCATCAAA GAAAGCCGGA 360

GGACACATCA AGAGGTACCT TCCATCGGGA GTTTGGCAAC GACGTANACC GAAGCCATGC 420

TGTGGAAGCC ANCAAAGTCG ACCTTTGTCG TCAAGCAACA AATTANAAGG GCTGTTGAGG 480

CATCGGGGAT CCCTTACACC TTTGTTATCT TCCAACTTCT TCGGTGGGTA TNTCCTCCCC 540

GTATTGGGAC AGGCANGAAC CACTGGTCCT CCCCACGGAC AAGGTTGTCN TCTTAGGTGA 600

ACGGGAACAC CAANGCGATC TTTCTCAATG AAAGACAACT CGGGACATNC CCNATTTAAC 660

CANTGGATGA TCCNANAACC TGAACAAGGT CTATTTCTGA AAACTTCNCC ATCTTCTTTT 720

TCTCATAACG AACCCNTTTN CCTCTT 746

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 795 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGCACGAGGA AANGAGATAA TCGTTGACCG AGGCAGAGAA TGGCGAGCGA GAAGAGCAAA 60

ATCCTGATCA TCGGGGGCAC CGGGTACATC GGCAAGTTCA TCGTGTTTGC GAGCGCCAGG 120

TTAGGTAACC CTACCTTCGC TCTCGTCCGG AGCACCACCG CCCCCGCCGG CCAACCCGAG 180

AAGGCCAAGC TCCTGAGCGA CTTCCAGGCC GCCGGCGTCA CCCTCGTCCA GGGGGATATA 240

TATAACCACG AGAGTCTGGT TAAGGCGATC AAGCTGGTGG ATGTGGTCAT CTCCCCCGTC 300

GGCTTCGGGC AGCTGAGTGA TCAGACCAAG ATCATCGACG CCATCAAAGA AGCCGGAGGA 360

CACATCAAGA GGTACCTTCC ATCGGGAGTT TGGCAACGAC GTTANACCGA AGCCATGCTG 420

TGGAGCCAGC AAAGTCNACC TTTGTCGTCA AGCAACAAAT CANAAGGGCT GTTGANGCAT 480

CGGGTNTCCC TTACACCTTT GTATCTTCCA ACTTCTTCGG TGGGTATTTC CTCCCGGTAT 540

TANGACAGGC AGGACCACTG GTCCTCCCCA CNGACAAGGT TGTCNTCTTA GGTGACNGGA 600

ACACAAAANC ATCTTTCTCN ATGAAGACAA CTCCGGACAT ACNCNATTAA AGCNGTGGAT 660

GATCCCAAAA CCTGAACAAG TTCCTATNTC TTGAAAACTT TCCCGCCCAA CCATCCTTTN 720

GTTCTCCCNT TAAACCNAAC CTCCATTTTC CCCTCCTTGG GGAAAAAAAA AAGGTCCGGC 780

NAANAACTTC CNAAA 795

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 797 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CGGCACGAGG NAGAACCTTT TGACAGAGTT GTTGTCATGG CAACAAAAGC TTCTCTCTCC 60

ATAAAAGGCT TTGCCTTGCT GGTTTCAGTC CTTGTAGCAG TTCCAACAAG AGTGCAATCG 120

ATTGGTGTCT GCTACGGCAT GCTCGGCAAC AATCTTCCCC CGCCCAGCGA GGTGGTCAGT 180

CTCTACAAAT CCAACAACAT CGCGAGGATG AGACTCTACG ATCCAAACCA AGCCGCCCTG 240

CAAGCCCTCA GGAACTCCAA CATCCAAGTC CTGTTGGATG TCCCCCGATC CGACGTGCAG 300

TCACTGGCCT CCAATCCTTC GGCCGCCGGC GACTGGATCC GGAGGAACGT CGTCGCCTAC 360

TGGCCCAGCG TCTCCTTTCG ATACATAGCT GTCGGAAACG AGCTGATCCC CGGATCGGAT 420

CTGGCGCAGT ACATCCTCCC CGCCATGCGC AACATCTACA ATGCTTTGTC CTCGGCTGGC 480

CTGCAAAACC AGATCAAGGT CTCGACCGCG GTCGACACGG GCGTCCTCGG CACGTCCTAC 540

CCTCCCTCCG CCGGCGCCTT CTCCTCCGCC GCCCAGGCGT TACCTGANCC CCATCGTGCA 600

GTTCTTGGCG ANTAACGGAA CGCCGCTCCT GGTCAATGTG TACCTTATTT TAACTACACC 660

GGCAACCCGG GANAGATCTC GCTGCCTACN CCCTGTTCAC GGCCNCGGGG TCTCNTGCAG 720

GATGGGCGAA TTCCNCTATC ANAANCTGTT CANTCCATCT TCNAAACCGG TCTTCCCGGG 780

CTGGAAAAAA TTGGAAG 797

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 792 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGCACGAGGA GAACCCTTTT GACAGAGTTG TTGTCATGGC AACAAAAGCT TCTCTCTCCA 60

TAAAAGGCTT TGCCTTGCTG GTTTCAGTCC TTGTAGCAGT TCCAACAAGA GTGCAATCGA 120

TTGGTGTCTG CTACGGAATG CTCGGCAACA ATCTTCCCCC GCCCAGCGAG GTGGTCAGTC 180

TCTACAAATC CAACAACATC GCGAGGATGA GACTCTACGA TCCAAACCAG GCCGCCCTGC 240

AAGCCCTCAG GAACTCCAAC ATCCAAGTCC TGTTGGATGT CCCCCGATCC GACGTGCAGT 300

CACTGGCCTC CAATCCTTCG GCCGCCGGCG ACTGGATCCG GAGGGAACGT CGTCGCCTAC 360

TGGCCCAGCG TCTCCTTTCG ATACATAGCT GTCGGAAACG ANCTGATCCC CGGATCGGAT 420

CTGGCGCAGT ACATCCTCCC CGCCATGCGC AACATCTACA ATGCTTTGTC CTCGGCTGGC 480

CTGCAAAACC AGATCAAGGT CTCCGACCGC GGTCGACACG GGCGTCCTCG GCACGTCCTA 540

CCCTCCCTCC CGCCGGNGCC TTCTCCTCCG CCGCCCAAGC GTNCTGANCC CCATCGTGCA 600

NTTCTTTGGC GAAATAACGG ANCGCCGCTC CCNGGTCCAT GTTTTTCCCT TATTTTAACT 660

ACNCCGGCAA CCCNGGAAAG ATTTCGCTGC CCTTACGCCC CCTGGTTTCC NNGGGGCTTC 720

CCGGGCGTTT CTTCCTTTGC CAGGGANTNG GGGCGAATTC CCNNCTTTTC CANAAACCTT 780

GTTCCAACNC CC 792

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 855 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CGGCACGAGT CTCTCTCTGT CTCTCCGTCG TCTCGTTGTC TGTTCGTTAG GGCTTGCGAT 60

CGCCACCGGT CGCGAGGGTT GGAGCCATGG AATTCTTGCG GTTTGGGGCT GAGGTGGCGG 120

CAGGAGAGGA AGCCGCGACG GGGTACTGGA TGCGATGGCA GACGCTCGTC TGCGCTCTGA 180

TCGTCGTCGC CCCGGCGGTC GCCGCGGTGG TTGTCGCGGC GCGGGCGCCG GCGCCGGCGC 240

GACCGCTCAG GGCCGTCGAT CTCTGGGCGC CGTGCTGGGC CGGGATGCAC CCGGCCTGGC 300

TTCTCGCGTA CCGCGGCTTC NTGTTCTTGG CCATGGCGTG GCTACTCTTC CANATGATTC 360

TGTTTCGCGG ATTCTCCGCG TTCTACTTCT ATACTCAGTG GACGTTTGCC TTAGTCATTG 420

TCTATTTTGC GATCGCAACC ATTATATCCG CCCATGGCTG CTGGCTTTAC TCAAAGAGAA 480

GTATTATGCC AGATCAGGAG GTCAACAGAT TCCTAAATGG TGGTTTTGAG CANAATAGTC 540

CTATGACTCT ACCTTTGAGG ACCAACAAAA ATATGAATGT TATAAGATTG CAAAGCTATC 600

NTGAACAGGA NGCTGATGAA NAAAAANCTG GATTTTGGGG TCCTGCTATG CNACTNGTCT 660

ATCAAAACCA TTGCANGTGC TGTAATTGTT GAAANACATT GTATTTTGGG NTCNTNCTAA 720

TACCATATTT GTCTTCTATA AATTTCAGGC TAAATGCTAT AATGGGCTGC ATGCATTCTC 780

TTAATGCTGT GTTTCTTCNA ATCCAACACT TTTCTCAATA ACCTGCCATT CCCNTNTTTC 840

NAATGGCATT TTTGC 855

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 722 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U31

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CGGCACGAGA GAGAGAGAGA GAGAGAGAGA GAGAGAGAGA GAGAGAGAGA GAGAGAGAGA 60
GAGAGAGAGC CTAGACCGGC ATCNTCGTGC TTGCCGAGGG GCGGCTTATG ANTCTTGGTT 120
GTGCCACTGG GCATCCCAGC TTCGTCNTGT CCTGCTCCTT CACCANCCAN GTGATNGCAC 180
NACTGGANTT ATGGANGGAA ANGGCGACCG GCNNGTACGA NAAGAANGTC TATGTGCTGC 240
CCANGCNTCT GGATGAGAGG GTGGCNGCGC TCCNCCTCGG CAAGCTGGGT GCCNCGCTCA 300
CCNAGCTTAC NCCNTCGCGG GCTGATTACA TTAGCGTCCC GATCGAGGGA CCCTACANGC 360
CTGCTCACTA CNGGTATTNG GGTTGCTTNT GCNAGAGACG ATGATNATAN NTCGGAGCAC 420
TGGCNTTTTC GACTANNAGT TTGACCGATG GCTATGTTCG TTTTGCTTTT CACCTTTTGT 480
CTTCCCATCT TTGCTGGTTC ACCTATGGAC GTTTGTTCCA TTTGGATGTN NTGAGAAATG 540
CTGATGGCAT TTTCGGAAAN AAAAANATNT AAAATCNCGA GAGTTCTTCT ANAGCGGCCG 600
CGGGCCCNTC NNTTTTCCCC CGGGTGGGGT ACCANGTTTG TTGTNCCCNT TCCCCCTNTT 660
TGAGTCCTTT TACTNCCCCT GGCCGTCGTT TTATACNTCG TTGACTGGGA ANACCCTGCC 720
NT 722

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 793 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGCACGAGCC TTGCCCAACT CCTTCGATTC GTTCCAACGA TCGGAGAATG GCGCTGCTGG 60
TGGAGAANAC GTCGACGGGA CGCGAGTACA AGGTGAAGGA CCTTTCTCAG GCTGACTTCG 120
GCCGCCTCGA GATCGAGCTG GCGGAGGTGG AGATGCCGGG CCTCATGGCG TGCCGCGCCG 180
AGTTCGGGCC CGCCAAACCT TTCGCCGGCG CCCGCATCTC CGGCTCCCTC CACATGACCA 240
TCCAGACCGC CGTCCTCATC GAGACCCTCA CCGCCCTCGG TGCTGAAGTC CGGTGGTGCT 300
CCTGCAACAT CTTCTCCACC CAGGACCACG CCGCTGCCGC CATTGCCCGC GACTCCGCCG 360
CCGTCTTCGC CTGGAAGGGA GAGACCCTCG CCGAGTACTG GTGGTGCACC GAGCGATGCC 420

TCGACTGGGG CCCCAACGGT GGCCCCGACC TCATCGTCGA CAAAGGGGGT GACGCCACTC 480

TCCTCATCCA CGAAGGCGTC AAGGCTGANG AAGANTACGA AAAAGACCGG CAAGCTGCCC 540

GATCCGGCCT CCACGGAAAA CGCCGAATTC CAAATCGTGC TGGGGATTAT CCGCNANCGG 600

CTCCAGGTCN AACCCCNAAA ATTACCGCCC AGATNAAAGA ACCCTCCTCC GCTTTTTGAA 660

GAAAACANCN CTGGCGTTCA NCGAATCTAC CANATGCCAG GGCCANCNGG GGCCCCTTGC 720

TTCTTTCCCC CCNCCCANTC NAACNTTCCN ACGAATTCCC GTTTTACCCN AAAAACCAAN 780

TTTTGAACAA CCT 793

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 847 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U32

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CGGCACGAGG CGACGCCGGC CTTCGCCTCC GCGTCTCCCT CCACCTCCAC TGCCACCGCC 60

GCCCTCGCCT CCCCCTCCCC AAATCGGTCG ACTCCGCCGC CGCTACAGAC CCCGACATCC 120

TATTCACTGA CCGCGCCGGC CGCCGCCGTG CCGACTGCCT CTCCTTCGCT GTCGACGACC 180

TCCCTGTCCT CGACGGCAGG ACCCCGATGG AAGCCTACGA GGAGTTCTTC CGGAGCTTCC 240

GCCTCGCCTT CGCTGACTTC TTTGGTTCCG TCATTACGGA TATCACGATC GGTCTCGGGC 300

CAAATGGCGA GCTCCGTTAC CCTTCGTTTC CTCCCACTGG AAGCAATCGT TTCACCGGTG 360

TAGGAGAATT CCAGTGTTAT GACAAATACA TGCTTGCCGA TCTCAAACGA CACGCGGAGG 420

AAACCGGCAG CCCATTATGG GGCCTCTCTG GTCCTCACGA TGCCCCTGGG TACAACCAGT 480

CTCCGGACTT CGGCAACTTT TTCAAGGACC ATGGCGGCTC CTGGGANACA CCCTACGGGC 540

AATTCTTCCT CTCCTGGTAC ACCGGCAAGC TCCTGTCTCA CGGTGACGGC CTGCTCTCGG 600

TCGCGTCAGA AGTATTGGTG ATTTGCCTGT CGCGCTCTCG GGCAAGGTTC CACTTTCTGC 660

ATTTGTTGGC AACGAAACTC GGTCGCGCCC GTCTTANCTT GAAGGCCGGG TTCTNTNACA 720

CTTGACGGNA NAANAACNGG TTTCAAGGAT GTTGGCTAAN ATCTCCCGAA ANCNTCCTGC 780

ANCATGATTC ATCCCGGGCN TGGACTTCTC NGAAGGGGAA CANTCCTCAG GGTGTTCCGG 840

TCTGCCC 847

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGCACGAGGC ATGGAGAACC CTGTTGCGAT GGGCATCATG GAGGAGCTTG AGGCCCAGAG 60
CGAGGTGTGG AACCACATTT TTAGATTCAT CACCTCCATG TCCGTCAAGT GCGCGGTGGA 120
GCTCAGGGTC CCCGACGCCA TCCACGCCCA CGGCGGCAAC GCAACTCTCC CTCAGCTGGC 180
CGCCGCCCTC AGCCTCCCTC CCGCCAAGCT CGCCGACCTC CGACGCCTCA TGCGCATGCT 240
GGTCCACGCC GGCTGCTTCG CCAAGCAGGA AGACNACGTG TACGCCCTCA CGCCATGGTC 300
GAGGCTCCTG NTGAGCTCCG AGCACACCGC GGTAGCCCCG TTCGTGGTGT GGATGCTCCA 360
CCCGCTCATG GTGCAGTCGT GGCACTCGCT GGGGGCGTGG TTCCACGGGA GGGCGCCCAC 420
CCCCTTCGCC GCAACCCACG GGAAAGGGGA TCTTCGAGAC NACACNCNAA CAGCCGGGGT 480
TCGCGGCCGT TCTTCANCNA NGCNATGGCG AACGACTGTC GGCTGGTGGG AAAGGTGTTG 540
GTAAANAACA TNCGGATGTG TTGGANGGAN CNCNGGTCCA TNGTGGAAGT TGGTGGCGCA 600
CCGGCACCCT TTTNGGCCAT TGTTGGCCGA AGGCTTTCCC GCCAACATNA AATNGCACCG 660
TTCTCCNANT TTGCCCCACT TTTCTGGCCN CNGCCGCCGG GGCCCCCNCN NACCNAAACA 720
ACTTGGATGT TTTTNGGGGG AANACATNTT CCAACATTTT ACANCCGCNC GACNTTTTTT 780
ACNCAATTGG TTCCNGGCNC NAATGGAAAT ANTNCTGNAT TT 822

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 743 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGCACGAAGA GCCCTGTACC GGANAGCATG GAGAACCCTG TTGCGGTGGG CATCATGGAG 60
GAGCTTGAGG CCCAGAGCGA GGTGTGGAAC CACATTTTTA GATTCATCAC CTCCATGTCC 120
GTCAAGTGCG CGGTGGAGCT CAGGGTCCCC GACGCCATCC ACGCCCACGG CGGCAACGCA 180
ACTCTCCCTC AGCTGGCCGC CGCCGTCAGC CTCCCTCCCG CCAAGCTCGC CGACCTCCGA 240
CGCCTCATGC GCATGCTGGT CCACGCCGGC TGCTTCACCA AGCAGGAANA CNACGTGTNC 300
GCCCTCACGC CATGGTCGAN GCTCCTGGTG AGCTCCGANC ACACCTCGGT GGCCCCGTTC 360
GTGGTGTGGA TGCTCCACCC GCTCATGGTC CAGTCGTGGC ACTCNCTGGG GGCGTGGTTC 420
CACGGGAAGG GCGCCCACNC CCTTCNCCNC NACCCNCGGG AAGGGGATCT TCCANACGAC 480

ACNCGAACAT CCGGGGTTCG CGGGCGTCTT CAACTANGCG ATGGCGAACG ACTGTCNGCT 540

GGTGGGAAAN GTNTTGGTAA AAAAACCTTC CGGAAGTGTT NGANGGAACC CCGTCCAATN 600

GTGGAANTTG GTGGCNGCCG GCACCCTTNC GGGCNATCGT TGTCGAAGNC CTTCCCNCAC 660

NTTANATTNC ACCGTCCTCC AATTNTCCCC ANTTTCTTTN GCCGCNGGNN NCGGGCCCCN 720

GGTNANCCNA AANCNTTTNT TTT 743

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 806 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TGTTCTCTCC TTCGATCACA TCTTTTTGCT CTGGGAAACG TGAGAGGTGA GACGAGGGCG 60

GCAATGACGG CGGGTTTAAG ATGGATTCCT CCTCTGCTTC TTCTTCTTCT GGGCTTCCTG 120

CTGGTTTTGA ACGGAGGTCG GGGGTGGATT GGAAGCGAGA GGTCCTCTGG CTCGAGGAAT 180

GGCGGAGCAT CGCGGAGGAG CTTGAGAGAG GCCTCCGCGA ACGCGACCAG CGCCGATGCT 240

TCCTTGGAAG AGAGGGCTGT AACCCGGGCA GCAGAAGCCG CAGTCGACGA CCCCGAGGAG 300

GTTGCTTCGA CGGTCCTGAT GACCATAATC AACAGCACGG CTCGCAGATC TCTTGGTTAT 360

CTGTCGTGCG GTTCAGGCAA CCCGATCGAC GACTGCTGGC GGTGCGACCC TGATTGGCAT 420

GTCAACAGAA AAAAGCTCGC TGACTGCGGC ATTGGCTTTG GACGCAACGC NATANGTGGC 480

CGCGACGGGG AATTTGTTCG TTGTGACAGA CTCCGGGGAC NATGATCCCC GTGAATCCTC 540

GCCCGGGAAC ACTTANATAC CCCGTCNTCC AANGAAGTTG CCCCCTCTGG GATCCCCTTT 600

AAACNCNAAN TGGAAATCTC NCTCNANGGA AGAACTCNTT ATGAACAGCT TTAANACNAT 660

CGATGGACNC NGTGTCCTCG TCCACATTGC CAATGGCGCC TGCNTCACCA NCCAATTTCN 720

TCCCCAACNT CTTCTTCCNT NGCCTCCNCT CCCCAATGCA ACCCNCCGGG AATTCCTNGT 780

CCCCNCTCCC CTTCTCCTAT GGATNG 806

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 687 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGCACGAGGG AGAACAAAAA TGGCAGCATT CTTGTTCTTC CTCACCATCG CAGCCTTCAC 60

TGCCCCCATC TACTCTTCTC GTGCACCCTT AACGTCGGCA GCTGTCCGCG ACCCTGAATT 120

AGTAGTACAG GAAGTACAAA GAAGCTTGAA CGTGTCGCGG CGGCGACTGG GCTACTTGTC 180

ATGCGGCACC GGCAATCCGA TCGACGACTG CTGGCGGTGC GACCCTGACT GGGCTGACAA 240

CCGGCAGCGG CTCGCGGACT GCGCCATCGG GTTCGGGAAG AACGCGATTG GGGGCAGGGA 300

CGGCGAGATA TACGTGGTGA CCGACAGTGG CGACNACNAC CCCGTCAATC CGAAGCCGGG 360

CACGCTCCGG TACGCCGTCA TCCANGAGGG AGCCGCTGTG GATCATCTTC AAGCGCGACA 420

TGGTCATCCA GCTGAAGGAA GGAGCTCATC ATGAAACTCC CACANAGACC ATCGACGGCC 480

GGGGCGCCAG CGTCCACATC TCCGGGGGGC CGTGCATCAC CACCAGTNCG TCNCCAACAT 540

CATCATCCAC GGGCGTCCAC TTCCACNAAT GCAANCAGGG CGGGGAACGC CTTACGTTCG 600

CGACTCCCCC AGGGCACTAC GGGTGGCGCA CCGGTGTCCG AACGGCNANG GGGTTTTCAT 660

CTTCCGCGGG AACCACTTCT GGGGTCA 687

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 741 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TCCACATTGC CAATGGCGCC TGCATCACCA TNCAGTACAT CACCAACGTC ATCATCCATG 60

GCCTCCACAT CCACGACTGC AAGCCCACCG GGAATGCCAT GGTCCGCAGC TCTCCTTCTC 120

ACTATGGATG GAGAACCATG GCTGATGGGG ATGCCGTTTC CATTTTCGGC TCCAGCCACA 180

TTTGGGTGGA CCACTGCTCT CTGTCCAACT GCGCCGATGG ACTTGTCGAT GCCGTCATGG 240

GCTCCACTGC CATTACGGTC TCCAACAATT ACTTCACCCA CCACAATGAG GTCATGCTTT 300

TGGGACACAC TGATTCTTAT GCAAGGGACA GCATCATGCA AGTAACGATC GCATTTAACC 360

ATTTTGGTGA AGGTCTGATT CAGAGAATGC CCAGGTGCAG GCATGGCTAC TTCCACGTGG 420

TAAACAATGA CTACACGCAC TGGGAGATGT ACGCCATTGG CGGTAGCGCG AATCCAACGA 480

TCAACAGTCA AGGCAACCGA TACCTTGCGC CGACCAATCC ATTTGCAAAG GAAGTAACAA 540

AAAGGGTGGA CACAGATCAA AGCACGTGGA AAAACTGGAA TTGGANGTCN GAAGGTGACC 600

TGCTTCTGAA TGGTGCTTTT TTCACCCTTC CGGTGCANGG GCTTTCACCC ANCTACGCAC 660

GGGCCTCCAC TTTGGGGGCA ACCCTCTTCC TTNGTTGANA CACTGACTCT GATGCTGGGG 720

TCCTGTTTTG CCAATTCGGN C 741

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 727 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGCACGAGTT CTCTCCTTCG ATCACATCTT TTTGCTCTGG GAAACGTGAG AGGTGAGAAG 60
AGGGCGGCAA TGACGGCGGG TTTAAGATGG ATTCCTCCTC TGCTTCTTCT TCTTCTGGGC 120
TTCCTGCTGG TTTTGAACGG AAGTCGGGGG TGGATTGGAA GCGAGCGGTC CTCTGGCTCG 180
AGGAATGGCG GAGCATCGCG GAGGAGCTTG AGAGAGGCCT CCGCGAACGC GACCAGCGCC 240
GATGCTTCCT TGGAAGAGAG GGCTGTAACC AGGGCAGCAG AAGCCGCANT CGACGACCCC 300
GAGGAGGTTG CTTCGACGGT CCTGACGACC ATAATCAACA GCACGGCTCG CAGATCTCTT 360
GGTTATCTGT CGTGCGGTTC AGGCAACCCG ATCGACGACT GCTGGCGGTG CGACCCCGAT 420
TGGCATGTCA ACAGAAAAAA GCTCGCTGAC TGCGGCATTG GCTTTGGCCC GCAACGCGAT 480
ANGTGGCCGC CACNGGGANT TGTNCNTTGT TGACAGACTC CGGGGACGAT GATCCCGTGA 540
ATCCTCCCCC GGAACACTTA ATATTCCCCG TCATCCCAGA NCTNCCCCTC TGGATCNCCT 600
TTTAAACACG ACATTGGAAA TCNCCCCCNG GAAGAACTCC TTTNTAACCG CTTTNNAACA 660
TCNATGGACN CGTGTCCACN TTCCACNTTT GCCAATGGCG CCTGCCTCNC CANCCNATTT 720
AATCNCC 727

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 842 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GGCACGAGGG AGAACAAAAA TGGCAGCATT CATGTTCTTC CTCACCATCG CAGCCTTCAC 60
TGCCCCCGTC TACTCTTCTC GTGCACCCTT AACGTCAGCA GCTGTCCGCG ACCCTGAATT 120
AGTAGTACAG GAAGTACAAA GAAGCTTGAA CGTGTCGCGG CGGCGACTGG GCTACTTGTC 180
ATGCGGCACC GGCAATCCGA TCGACGACTG CTGGCGGTGC GACCCTGACT GGGCTGACAA 240
CCGGCAGCGG CTCGCTGACT GCGCCATCGG GTTCGGGAAG AACGCGATTT GGGGCAGGGA 300

CGGCGAGATA TACGTGGTGA CCGACAGTGG CGACNACGAC CCCGTCAATC CGAAAACGGG 360

CACGCTCCGG TACGCCGTCA TCCAGGAGGA GCCGCTGTGG ATCATCTTCA AGCGCGACAT 420

GGTCATCCAG CTGAAGGAGG AGCTCATCAT GAACTCCCAC AAGACCATCG ACGGCCGGGG 480

CGCCAGCGTC CACATCTCCG GCGGGCCGTG CATCACCACC AGTACGTCAC CAACATCATC 540

ATCCACGGCG TCCACATCCA CGAATGCAAG CAGGGCGGGA ACGCGTNCGT TCGCNACTCC 600

CCAAGGGCAC TACGGGTTGG CGCACNGTGT TCNGACGGCG ACGGGTGTCC ATCTTCCGCG 660

GGAACCACTC TGGGTCCAAC CACTGCANCG CTTGTTCCAA CTTGGCCCAC CNAANTGGGC 720

CTTCCNTCCC AACCCCCATT TCCTTGGGAT TNCCCCCCGC CAATTCCCCC ATTTTCCAAC 780

NAACTTNCTT TGAACCCNCC CNTGAANAAG GTCCTTGCTG CTGGGTCCCA CCAACAATTT 840

NA 842

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 724 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GGCACGAGTC TCCTTCGATC ACATCTTTTT GCTCTGGGAA ACGTGAGAGG TGAGACGAGG 60

GCGGCAATGA CGGCGGGTTT AAGATGGATT CCTCCTCTGC TTCTTCTTCT TATGGGCTTC 120

CTGCTGGTTT TGAACGGAGG TCGGGGGTGG ATTGGAAGCG AGAGGTCCTC TGGCTCGAGG 180

AATGGCGGAG CATCGCGGAG GAGCTTGAGA NAGGCCTCCG CGAACGCGAC CAGCGCCGAT 240

GCTTCCTTGG AAGACAGGGC TGTAACCAGG GCAGCAGAAG CCGCAGTCGA TGACCCCGAG 300

GAGGTTGCTT CGACGGTCCT GACGACCATA ATCAACAGCA CGGCTCGAAN ATCTCTTGGT 360

TATCTGTCGT GCGGTTCAGG CAACCCGATC GACNACTGCT GGCGGTGCGA CCCCGATTGG 420

CATNTCAACA GAAAAAAGCT CGCTGACTGT GGCATTGGCT TTGGCCGCAA CCCGATANGT 480

GGCCGCGACG GGGANTTGTN CGTTGTGACA GACTCCGGGG ACGATGATCC CCNTGAATCC 540

TCCCCCGGGA ACACTTANAT NCCCGTCNTC CNNGAANTTT CCCCTCTGGA TCNCCTTTAA 600

ACCCACNTGG ANATCCCCCN CNAGGAAGAA CTCCTTATGA ACNGCTTTTT AAAACATCGA 660

TNGGACCCNG TTTCCACTTC CNCATTNGCC NAATTGGGCG CCCTGGCCNT CCNCCCNTCC 720

CCAA 724

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 797 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGCACGAGGG ACAAGCGATG GCAGCAGAAT TGTCTCCCAC GCTGAGCAAG AGCATCTTTG 60
AAGGAGCCGG TGGATCTTAC TCTACTTGGT CAGGTGCCGA TCTCCCCCTT CTTACTGATG 120
CAAAGCTCGG CGGAGGCAAG CTTGTCCTGA AACCACTGGG CTTGGCGTTG CCTCACTATT 180
CCGACTCATC GAAAGTCGGC TATGTTCTTG AAGGAAGAGC GGTGGTGGGG CTAACACTCT 240
ATGGAGAGAC CGAGCAGAGG ATACTGCTGC TTGAGAAGGG AGATGTGGTA GCGGTGGTCA 300
TGGGGAGCCT CACGTGGTGG TACAACGAGG AGGAGGACTC CGACTTCTCC ATCGCCTTCT 360
TAGGCGATAC CGCGACAGCT GTGCGACCGG GCGACATCGC CTACTTCTTC TTGGCAGGAT 420
CCCTAGGAAG TGCTCCATGG CTTTTCGACG GAAATTCCTC ANCAGGGCCT GCGGTTTAAG 480
GGGATGCGGA AGCTGANGAG CTCTTCGGAA GCCAACCTGG TACTCTAATC ATCACACNGC 540
AGCAAAAGCT GCCTGGCCTC AGANCATCCC GAGCTGACAG CNAAGGGATA TCNTAAACGC 600
TGANCGCGTA NCGGCATATA TCAATGTGAA AAGTGGTGGC TGTTCTGCCT CGGTGACCCT 660
TNATNAACTG GCNGCNCTGG GAAGATCAGG TTCTCCGTCN ACCTCCAAAA ATCCANCCTA 720
ACCCCGTGCC TTGCCGGGGT TCTTCNTTGA ATCNNCTGTT CANCTGAAAT TTTTCCCCAA 780
GGCCNTGGAA CAATTCT 797

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 742 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GGCACGAGAT GACTCTCTCG GCGGTAGCAT CGGATGCCGA TGATTCGGTC GCTTATACAT 60
TCGCTTCGCG ATACGTTCGC GAGGCTCTTC CCCGGTTCAG GATACCGGAG CAGTCGATCC 120
CCAAGGATGC GGCGTACCAG ATCATCAACG ACGAGCTGAT GCTCGACGGG AACCCGCGGT 180
TGAATCTGGC GTCGTTCGTG ACGACGTGGA TGGAGCCGGA GTGCGATCGC CTCATCATGG 240
CGGCCGTCAA CAAGAACTAC GTCGACATGG ACGAGTACCC CGTCACCACC GAGCTCCAGA 300
ATCGCTGCGT AAATATGATA GCCCACCTTT TCAATGCCCC AATTGGGGAA NACGAAACGG 360
CTGTTGGAGT TGGAACTGTG GGTTCCTCCA GAAGCAATCA TGCTTGCAGG ACTTGCATTC 420

AAGAGGAAAT GGCAGAACAA AAGAAAGGCA GAGGANAAGC CTTACGACAA ACCCAACNTT 480

GTTACCGGTG CAAATGTTCA GGTTTGCTGG GANAAATTTG CAAGGTATTT TGAAGTTTGA 540

ACTGAAAGAA ATTGAAGTTG AAAGAAGGAT ATTATGTTAA TGGATCCTGC CAAGGCAGTA 600

NAAATGGTTG ATGAAAAATA CATATGTTTT TGCTGCCATC TTTGGGTTCA ACTCTCCCTG 660

GGAAAATTTG AANATGTTAA CCTTCTAAAT GATCTCCTGA CNGAAAAAAA CCCAGAAACT 720

GGGTTGGACC CCCCNTACTT GT 742

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 807 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GGCACGAGCT CTAGCCGATG ACTCTCTCGG CGGTAGCATC TGATGCCGAT GATTCGGTCG 60

CTTATACATT CGCTTCGCGA TACGTTCGCG AGGCTCTTCC CCGGTTCAGG ATACCGGAGC 120

AGTCGATCCC CAAGGATGCG GCGTACCANA TCATCAACGA CGAGCTGATG CTCGACGGGA 180

ACCCGCGGTT GAATCTGGCG TCGTTCGTGA CGACGTGGAT GGAGCCGGAG TGCGATCGCC 240

TCATCATGGC GGCCGTCAAC AAGAACTACG TCGACATGGA CGAGTACCCC GTCACCACCG 300

AGCTCCAGAA TCGCTGCGTA AATATGATAG CCCACCTTTT CAATGCCCCG ATTGGGGAAN 360

ACNAAACGGC TGTTGGAGTT GGAACTGTGG GGTCCTCAAA AGCAATCATG CTTGCAGGGC 420

TTGCATTCAA GAGGAAATGG CANAACAAAA GAAAGGCAGA GGANAAGCCT TACGACAAAC 480

CCAACATTGT TACCGGTGCA AATGTTCNGG TTTTGCTGGG AANAAATTTG CAAGGTATTT 540

TGAAATTTGA ACTGANAGAA NTGAANTTGA AAGAAGGATA TTATGTTTAT GGATCCCNGC 600

CCAAGGCAGT ANAAATGGTT GATGAAAATA CCAATTTNTG TTGCTTGCCC ATCTTTGGGT 660

TCCACTCTCN CTGGGANAAT TTTGAAAAAT GTTNAGCTTC TAAATGATCT CCNGGACCNA 720

AAAAANNCCC NNAANCTNGG TTGGGACCCC CCCNTACCTT TTCNATNCCT GCCANTTNGG 780

GGATTCNNTA NCGCCTTTCC TNCTATC 807

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 770 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: U-U91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GGCACGAGAG AAAAAATTGT AAAGTTTGAC TTTCATGGAC AGCCTGCGGA GCTCAAGCAT 60

GGTAGCCTTG TCATAGCAGC AATTACAAGC TGCACAAACA CATCAAATCC CAATGTTATG 120

CTTGGTGCTG GTCTTGTTGC AAAGAAGGCC TGTGAATTAG GTCTACAGGT TAAGCCTTGG 180

ATCAAAACCA GCCTTGCTCC AGGTTCTGGA GTTGTTACCA AGTATTTGCT TAAGAGTGGC 240

CTACAAGAAT ATTTGAATCA GCAAGGATTT AATATTGTTG GGTATGGCTG CACAACATGT 300

ATCGGAAACT CTGGGGATCT TGATGAGTCT GTGGCTGCTG CAATTTCCGA TAATGATATA 360

GTTGCTGCTG CTGTTCTATC TGGAAATAGG AATTTTGAGG GACGTGTGCA TCCATTGACA 420

CGAGCTAACT ATCTTGCTTC ACCTCCGCTT GTTGTAGCTT ATGCGCTTGC TGGAACAGTT 480

GACATTGATT TTGAAAAAGA ACCCAATTGG AACAGGGGAA GGATGGGAAA AAACATATAC 540

TTCCAGGATA TATGGCCGTC CACTGAANAA ATTGCACAGG TTGTGCAATC CANTGTTTTT 600

GCCTGAAATG TTCAAGAATA CCTATGAAGC AATCACCAAA GCACCCTATG TTGGAACCAA 660

CTGACTGTTC CCNGCCACAC TCTTTATTCA TGGGACCCAA TCCNCNTACA TCTTAACCAC 720

CNTATTTTAA GGANATGACC ATGGCCCNCC TGTCCNCATG GGGTGAAAAA 770

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 810 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GGCACGAGAG GGCCGTTCCT TTTTGTGCTC GCTTTGCTGC CTCCTCGTTC GTCTTTTCCG 60

CGAATTTCAC CGGCCATGAA CAGCCTTCGG AGCCTTCCGA CATCCTCCGC TCCGCCCTCG 120

CCGGTCCCGA GAGGACGTTC GAGTAGGCCA CCGACCTTGA ATCTGGGGGT GATACGACCA 180

CATCATCTTC GTGTAAATGT CGCCAGGAGT GCATGTTCCA AGTCTTCTGC AAGTCCTGAG 240

AAGACTGGTG CTGAAGTGCA AGATCAGAAG TCTGAGATAT ATAGCAGTGA TATGACAAAA 300

GCAATGGGTG CAGTGCTGAC ATATAGGCAT GAGCTTGGAA TGAATTATAA TTTCATCTAC 360

CCAGGATTGA TTGTTGGTTC TTGTCTACAG ACCCCATCAG ATGTTGATAA GCTTCCNAAA 420

GATTGGGGTT GAAGACCATC TTTTGCTTGC AGAAGGACTC GGATCTTTGA ATATTTTGGG 480

GTTGAAATTG GTGCAATTCC NTGAATATGC CATGCAATGT GGTGACATTG AACATCTTCN 540

TGCTGAAATC AGGGATTTTG ATGCATTTGA TTTGAAGATG ANACTTCCTG CNGTANTTAC 600

NAATTATACA AGGCTAATTA ATCCGAATGG TGGAATGACT TATTTTCNCT GTACANCCNG 660

GCTTGGAAAA CGCCTGCANT TGCNTTGGCA TACNTGTTTT TGGGTTNAAG GCTATGAACT 720

GAATGAAAGG GCCCCNCTAC TGCNAAATTA NCCAACTTGC TCCCCNAAAT TTGGTGCTAT 780

AAAAANTGCC ACCNTTGATA TGCTTATNGG 810

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GGCACGAGCT TGGCTGTAGT CTTCTTCTCA AGTAATCTTC GTCTTCCTGA TTTGCTTGGT 60

TGGTGGTCGG TTGCAGGGCG AAGGGATGGG GATGGGGAGG CCGAGCGGAG CTTGGTCGAC 120

CCCGTGGTTG GTGGTGGTTC TTGTGCATTG GCTCCTCTGG GCCACCGAGA GGAGGCGAGG 180

GGCGGTGGTG GAGGCCTCCC ATGTGGAGTT TGCATCCCTC CAATCTGTTC CTGCCTCCGT 240

CGTCGACAAC AGGCTGAGGA CTGGGTATCA CTTCCAGCCC CCGAGGAACT GGATCAACGA 300

TCCAAATGGA CCCATGTACT TCAATGGCGT CTACCACCTC TTCTACCAGT ACAACCCCAA 360

TGGCTCCGTG TGGGGTAACA TCGTGTGGGC CCACTCGGTG TCGACCGACC TCGTCAACTG 420

GATAGCACTC GACCCGGCCA TCCGCCCCAG CAAGCCATTC CACATCAACG GATGCTGGTC 480

CGGCTCCGCC ACCGTCCTCC CCGGCAACAG GCCTGCGATC TTCTACACCG GCATCNACCC 540

CCANCANAAA CAACTGCANA ACNTTNCNTN CCCAAGGATC TGTCCAACCT TACTCCCCNA 600

NTGGGTCAAC CCCACTNCAA CCCCGTGATC CCCCTGGCGA CGCATCAACN CCACCCCTTC 660

CNCNAACCCN AATACGGNTT GGCGCNGTCC CNGCACCCNC TGGAAACCCC TNGTNGGGAA 720

CNANTTGAAN CNGAAGGGGA AAGGCNTTCT TTNCCGAACA GGGAT 765

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 774 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GGCACGAGCG GAGAANGCAA TCTCGCTCTC TCTCTACTGC ATCGCGGCTC TCGTCCTCGA 60

TTACTTGAGA TATGGCAGGA AAGGGCGAGG GGCCGGCGAT CGGGATCGAT CTCGGCACCA 120

CGTACTCGTG CGTCGGGGTG TGGCAGCACG ACCGGGTGGA GATCATCGCC AACGATCAGG 180

GGAATCGTAC CACCCCCTCC TATGTCGCCT TCACCGACTC CGAGCGCCTT ATCGGCGACG 240

CTGCCAAGAA CCAGGTCGCC ATGAACCCCA TCAACACCGT CTTTGATGCA AAGCGTTTAA 300

TTGGTAGGCG ATTCAGTGAT TCATCTGTCC AGAGTGACAT CAAGCTCTGG CCTTTCAAGG 360

TCATTCCTGG TCCAGGTGAC AAGCCCATGA TTGTTGTCCA ATACAAAGGG GAGGATAAAC 420

AGTTTGCAGC TGAAGATATT TCTTCCATGG TTTTGATAAA GATGAAAGAA ATTGCTGAAC 480

CTACCTGGGG TCTGTTGTCA AGAATGCCGT CCTCACTGTT CCCGCTTACT TCAATGACTC 540

NCAACGCCCA GCCACAAAGG ATGCTGGTGT CATTGCTGGT CTCNATGTTA ATGANAATCA 600

TCAATGANCC CCCAGCACTG CTATTGCTTT ATGGCCTTGA CAAAANGCTA CTATTGTTGG 660

TGAAAAAAAT TTCCTCATCT TCCATCTCCG GTGGGTGGCC TTTTGANTTC NCCTTCCTNA 720

CCATCCAAGA AGGTTTCTTT NAAGTCAAGG CCCTGCTGGT GANACCCANC TTGG 774

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 786 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GGCACGAGCT AGTCTCGAGT TTTTTTTTTT TTTTTTTTAA AATTGAAATT AGATGCGATT 60

TCGAATAGCA AACATAGTTC AGGATAAACC AACAACATTG TACCGAATTC GATAAGCTTA 120

GGAAACTAAA TTGCGTAAAC GAAACACTTG CATGAAAGCC TATATAATAT AAGGCCGACT 180

AGGGACNAAA TAACTTAATC GACCTCCTCG ATCTTTGGAC CAGCGCCGCT GCCACCAGCA 240

GGAGGAGCAT CATCATCCAT ACCACCAGCC ATGTCAGCAC CTGCTCCCTG GTACATCTTG 300

GCGATGATGG GATTGCATAT GCTCTCCAGC TCCTTCATCT TGTCATCGAA CTCGTCGGCT 360

TCTGCCAACT GGTTGCCATC GAGCCATTGG ATGGCCTGCT CGATCGCATC CTCCGATCTT 420

CTTCTTGTCA GCAGCAGCAA GCTTGGAGGC AATCTTGTCG TCGTTAATGG TGTTCCTCAT 480

GTTGTNAGCA TANTTTTCCA GANCATTCTT CCGATTCCAC CTTCCTTTTT ATGCTCCTCC 540

ATCTTCCTGA CTTGTTACTT CTCCGCTTCC CTGCACCATT TTCTCAATCT CCTCCTTGCT 600

GACCTACCTT GTCCTTGGTG AAGGTGATCT TGTTCTCTGT CCAGTGGTCT NTCNTCNGCA 660

GAAANATTCC AGAATACCAT TGGGGTTCCA AATGTTNCAA AACCAAACCC GGTGGATTCT 720

TGAAGGAAAC CCCCCCCTAA GGGCCCCAGG GTGGGAAATC CCCCCAAAAA ACCCCCAAAT 780

TTTCCC 786

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GGCACGAGCG AGTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTCACAAG GNAACCATAG 60

ACATTACACC AAACATAGAT GTCAACAATA CATGCCAACG ATACCATTGC TTATTCCTTC 120

AGACCTCCGA TAGGACTTCC ACGCACACCA ACAGAGAGAA CTAAGACAGC AAAGCAGCGG 180

ACACATACAG CCCAAAAGGG TNNGTGACCC CCGCGGAGGN GGAGCNCCAG GTGAAGGGTG 240

GATTCCCTCT GAATGTTGTA TTCTGNCAGG GTGCGCCCGT CCTCNNTTTG NTTCCCNTCT 300

NANATCNCCC NCTGNTGATC TGGTGGNAAT CCCCCCCTTG TCCTGTGATT CTTGCTCTTG 360

ACNTTTTTCT CCCNTGTCNN ANCTCTCTNC CTNCTCTGGG TNTTGGGTCT TCCCCTGTTG 420

NANCNNTCTN TTNNCNTATC ATCTTGTNCT CCNNCCNCCN CNCCTNTCNT TTCCTCNNNN 480

GGTNNA 486

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 791 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GGCACGAGTG ACAATGTCAA GGCCAAGATT CAGGATAAGG AGGGCATTCC CCCCGACCAG 60

CAGAGGCTCA TCTTTGCCGG CAAGCAGCTC GAGGATGGCC GCACCTTGGC TGATTACAAC 120

ATCCAGAAGG AGTCCACCCT CCACCTTGTC CTCCGCCTCC GTGGTGGCAT GCAAATCTTC 180

GTCAAGACTT TGACTGGGAA GACCATCACC CTTGAGGTGG ANAGCTCGGA CACCATCGAC 240

AATGTAAAGG CCAAGATTCA GGACAAGGAG GGTNTTCCCC CGGACCAGCA AAGGCTCATC 300

TTTGCCGGCA AGCAGCTTGA GGATGGCCGC ACCCTGGCAG ATTACAACAT TCAGAAGGAG 360

TCTACCCTTC ACCTTGTGCT GANACTTAGG GGTGGCATGC ANATCTTTGT TAAGACNCTC 420

NCAGGGGAAG ACCATTACCT TGGAGGTGGA NANCTCNGAC ACGATTGATA ATGTCNAGGC 480

AAAGATCCAN GACAAGGANG GGATTCCACC GGATCAGCAN ANGCTGATCT TTGCTGGGAA 540

ACACTGGANG AAGGGCGCAC CCTGGCAGAT TNCNACATTC CNAAAGAATC CACCTTCACC 600

TGGTGCTCCC CCTCCGCCGG GGTCCCTAAC CCTTTTGGGC TGTATGTNTC CCCTGCCTTT 660

GCTGTCTTAA TTCNCTCTGT TGGTGTTCGT TGGAAATTCC CTAATCCNGA AGGTTCTTNA 720

AAAGGAAATN AANCCNNTTG GGTTTTCCCC TTTGGCCTTT TTTTTGTTTG AAAATCCTNT 780

GTTTTTGGTG T 791

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GGCACNANCC CGCTTCGGTA GCCATTATTG GTGCCCGTAG AGCGAGTGCT GAGATGGCTT 60

TGAGGGCCTT CTTCCCCCTC TGCATCGCTC TCGTGGTGAC GCTCTCACCT CTGTGTGATG 120

CCACTTCGCC TTACTACACC ATCACACCGC CCACCCCCGT GGCCAAGCCG CCTTCAGTTG 180

AACCACCACC CTACCACGGC CCTCCGACNA CCCACCCTAA GCCACCGAGT CATGGTGGCC 240

AACCTCCGTC CCACCATCAC CCAACACCAA TCTACGGTGC ACCCCCTCCG CAACACCACC 300

ACCACCACCA ACACCACCAC CAACCTGCAC CACCAACTCA CGCANAACAC CCTCCGTACT 360

ACCACATGCC TTCCCCGCCG CCGCATGGCC AGCACCCGTC ACCACCGTCA CATGATTATC 420

CCGTACCTCC TGCTCACAAG CCCCGAACTC CGCCGCCGGT TTACAAGTCT CCACCACCGA 480

NCCACCGTCC TTACCCTCCA TCGACGCCAC CCCACCATCC GAAGCACCCG CCTTCTCAGC 540

CGAAGCCGTC NTACAAGGCC CGCCACCATN CAAGAACATC CCTGANCACT CTCCACCGCC 600

GCGTCACTAT CATTCTCCGT CTTCACCACC ACCACCACCA CCATACAAAA TAATCTCGTT 660

TTGCCATCTT CTCCCGTTTG AAAAAAAANN CAANTGTCCT TTTTATTTAA CCNAATCCAN 720

GGGGTTTTTN TTAANATTTN AANAAANCNA ANTNTTTTCC CCCCCNTNTT GGTTNATGGC 780

CTATGGGTTT GTTTCTCTTC TTGGCTTTTC CCGG 814

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 742 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GGCACGAGGT TGTGCCTAAC AGAGAGAGAG AGAGACAGAC CGATAGCCTC CTCATTCACT 60

ATGGCGATCC GATCGCCAGC TTCGCTGCTG TTATTTGCGT TTCTGATGCT TGCGCTCACA 120

GGAAGACTGC AGGCCGGGCG CAGCTCATGC ATTGGCGTCT ACTGGGGACA AAACACAGAC 180

GAGGGAAGCT TAGCAGATGC TTGTGCCACA GGCAACTACG AATACGTGAA CATCGCCACC 240

CTTTTCAAGT TTGGCATGGG CCAAACTCCA NANATCAACC TCGCCGGCCA CTGTGACCCT 300

CGGAACAACG GCTGCGCGCG CTTAAGCAGC GAAATCCAGT CCTGCCAGGA GCGTGGAGTC 360

AAGGTGATGC TCTCCATCGG AGGTGGCGGG TCTTATGGCC TGAGTTCCAC CGAANACGCC 420

AAGGACGTGG CGTCATACCT CTGGCACAGT TTCTTGGGTG GTTCTGCTGC TCGCTACTCT 480

CNACCCCTCG GGGATGCGGT TCTGGATGGC ATANACTTCA ACATCCCCGG AGGGAGCACA 540

GAACACTATG ATGAACTTGC CGCTTTCCTC CNAGGGCTAC AACGAACAGG AAGCCGGAAC 600

CAAAAAAGTT TCACTTGAAT TGCTGCTCCC NCANTGTCCT TTCCCCGATT ACTGGCTTTG 660

GCAACCCACT CCAAAACAAA TNTCTTCCNA CTTCCNTGTT GGGTTGCNAA NTTCCNTTCC 720

CAANCAAACC CCTTTCNTTT GC 742

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 794 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GGCACGAGGG CGTGGCGGAG ATGGGGAGCT GGCGGGCTCT GTTGCAGCGG CGGCTGCTGT 60

TGCTCTCTGC TTTGGCGGTG GCTGTTCGTG TGAAGGCACT CAGCANANAC NATTTCCCCG 120

CCGGCTTCAT TTTTGGCGCA GGCACCTCCG CTTATCAGGT ANAAGGTGCA GCTGCAGAGG 180

GGGGAANAAC ACCCAGCATT TGGGACACGT TTACGCATGC AGGGAGAACT TTCGACCAGA 240

GCACCGGAGA CGTAGCAGCT GATCAGTATC ACAAGTACAA GGAAGATGTG AANCTGATGC 300

ATGANATGGG CTTCGATGCT TACAGATTCT CCATCTCCTG GTCCANAGTT ATCCCCAATG 360

GTCGAGGGCC TGTGAATCCA CAAGGCTTGC GGTACTACAA CAACCTGATC GATGAGCTCN 420

AAAGATATGG AATCCGAGCC TCATGTCACT CTTTACCACT TCGACCTTCC GCAAGCACTG 480

GAANACGAAT NCGCCGGGCA GCTGAACCCA AAGATCGTAN ANGACTTCAC CGCTTACGCC 540

AACGTTTTGC TTCANCNAAT TTGGGGATCN AATCTAGCAC TGGATCNCCC ATCAATGAAC 600

CAACATANAT CCCGTCCTCC GCCACNAATT CCGCATCTTC NCCCCTGGCC CCTGCTCTTT 660

ATCCCTTNCG CCTCCAACTG CNCCAAGGGC NACTCCCCCC CATTTTNAAN CCCATNNNNT 720

CCNCCCCCCC CAATTAACCC NTTCTTGCTC TTCCCCCTTG CCTTCANCCA ACCCGCCCNT 780

TTTCCNAAAA AANA 794

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 799 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GGCACGAGCC GGCCTCAGGC ATATGGTGCG GTCGCTACAC GTGTTCAGGC AAGGCCGGGA 60

GCCGGCCAGG ATCATCAGGG AAGCACTGTC GAAGGCGCTG GTGAAGTACT ACCCCTTCGC 120

GGGGCGGTTC GTGGACNATC CCGAGGGCGG CGGCGAGGTT CGTGTCGCTT GCACTGGCGA 180

GGGCGCTTGG TTCGTCNAGG CCAAGGCGGA CTGCAGCTTG GAGGACGTGA AGTACCTCGA 240

TCTCCCGCTC ATGATCCCTG AGGACGCGCT CCTGCCCAAG CCCTGCCCGG GACTGAACCC 300

CCTCGACCTC CCTCTCATGC TGCAGGTGAC ANANTTCGTG GGCGGCGGAT TCGTGGTCGG 360

CCTCATCTCC GTCCATACCA TCGCCGACGG CCTCGGCGTC NTCCANTTCA TCAACGCCGT 420

CGCCCGAAAT CGCCCGTGGC CTGCCNAANC CCACCGTGGA NCCTGCATGG TCCCGGGANG 480

TCNTACCCAA CCCACCTAAG CTGCCTCCCG GTGGCCCGCC CGTGTTTCCC CTCCTTCAAN 540

CTGCTCCACG CCACCGTCGA ACTATCCCCT GACCACATCC ATCACGTCAA GTCCCCACAC 600

TTTGGANCTC ACCCGGCCAA CGCTGCTCTA CCTTCCACNT CCCCATCCCC AACCTGTTTG 660

NAATCCCGCA CGCCCCGCCN TCNACCTTGG AACCCAAGGC NTTTCCAANC TTTGCAACCC 720

TTTTTTCCTT TCCTTCCCCC CCCAAAANAA CTTCCCCCCA CCCTTGTTTT TGCNCCCAAG 780

TTTTTTCCTT CCTTGCCCC 799

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 759 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U43

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GGAGGTTGTT GTTCATGTCC CTACTTCGGG GTCTCCTGTA CAGATTGAAT TTCAAGTAAC 60

TAATAGCAGT GGCTACTTGG TGCTTCATTG GGGTGCAATT CATAATAGAA GGAATAACTG 120

GTCACTTCCT TCTCGTCATC CTGATGGAAC AAAAGTATAC AAAAACCGAG CTCTCAGGAC 180

ACCTTTTAAA AAATCTGGTT CCACATCATC AGTAAAAATG GAGATTGATG ATCCTGAAAT 240

ACAAGCAGTT GAGTTTCTCA TATTTGACGA GTCAGAAAAC AAATGGTTTA AACATAATGG 300

TCAGAATTTC CATGTCCAGT TATTAAAACA GGGCTATCAA AATCAAAATG TTTTGGCCTC 360

TGTAAATCCA AATGTTTCAC TGCCANAAAG AACTTGTGCA GATTCAAGCT TATCTTAGGT 420

GGGANANAAA GGGTAGGCAA ACATATACAC CTGATCAAGA AAAGGATGAG TNTGAAGCAG 480

CTANAACTGA GTTTGCTANA AAAACTAAGT NNAAGTACTT CTGTANANGA NCTCCGATCT 540

AAATTGACAA AAAACNCCAC TGCTGGAGCG GACAAATCCG TCAAAGTTGA AACTATCAAA 600

AGTGGGATCC GGATGATCTT NTGCAAGTTA CANGCATACT TCCNATNGGA AAAACCGGGA 660

AACCATNTTA TCCCCCNGAA AAACACTNAT GGAATTGAAG AAACCAGGGA AANACTGCCC 720

ATGAATTAAA TAAANGAACN CNCCTNCAAA CTNAGGGAA 759

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 785 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

GGCACGAGAG AGAGAGAGAG AGAGAGAGAG AGAGAGAGAG AGAGAGAGAG AGAGAGAGAG 60

AGAGTAATCG ATTTAGCGTG CAAAGTACTG CAGCAGAAGC CATGGCATCC ANGGCCTCAG 120

CNTCGGCTGC CCTCTTCCTT GCTCTCAACC TTGTCTTCTT TGCACTCACC AGTGCTTGTG 180

GCACCACTTG CACCCCCGCC ACTAAGCCCC CACCGAGCTC TTCCCATGGC AAATGCCCCG 240

TCGACACCCT CAAGCTGGCC TCCTGCGCCA ACGTGCTCAA TGGCCTGATC NNGGTCGGCG 300

TCGGCAAGCT CCCGAAACAG CCGTGCGAGT GCTGCNCTCT GCTCGATGGC CTCGTCGACC 360

TCGAGGCCGC CGTGTGCCTT TGCNCTGCTA TCANGGCCNA TGTCCTTGGC ATTCATCTCA 420

ACCTCCCCAT CNNCTTCAGC CNTCTCCTCA ACTACTGCGG TNAGAAGGCT CCCACCGGTT 480

TCCAGTGCCC TTGAGCTCCC CCTGCGGATC ACATCNTCGA TCCTCTTTGC CCGTGGTGAA 540

TTTTNTTGAG CATTCCTTTG TGTCTTTACT TCCCTTTGTT TTTGGCTTTT TGATGACGAA 600

AGTGTTGAGT GTTGATATGA AGGGCCANTG GCGCTTTCNT GTTAATGTTA CCTGTCNTTC 660

CCTTTTTATT TCCACNNCTT GTTGANTTTC CCTCTCGGGT TTGTTAATGA AGATCNATGC 720

ATTCAATTNT TAATATTTCT GCTGCCTTCC AANAAAAAAT ANNANTNCCT CCNNGAANTC 780

TTCCT 785

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 784 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CGGCACGAGG AAANGACNAG CGATGGCAGC AGAATTGTCT CCCACGCTGA GCAAGAGCAT 60
CTTTGAAGGA GCCGGTGGAT CTTACTCTAC TTGGTCAGGT GCCGATCTCC CCCTTCTTAC 120
TGATGCAAAG CTCGGCGGAG GCAAGCTTGT CCTGAAACCA CTGGGCTTGG CGTTGCCTCA 180
CTATTCCGAC TCATCGAAAG TCGGCTATGT TCTTGAAGGA AGAGCGGTGG TGGGGCTAAC 240
ACTCTATGGA GAGACCGAGC AGAGGATACT GCTGCTTGAG AAGGGAGATG TGGTAGCGGT 300
GGTCATGGGG AGCCTCACGT GGTGGTACAA CGAGGAGGAG GACTCCGACT TCTCCATCGC 360
CTTCTTAGGC GATACCGCGA CAGCTGTGCG ACCGGGCGAC ATCGCCTACT TCTTCTTGGC 420
AGGATCCCTA GGAGTGCTCC ATGGCTTTTC GACGGAATTC CTCANCAGGG CCTGCGGTAT 480
AAGGGATGCG GAANCTGAAG AGCTCTTCGG AAGCCAACCT GGTACTCTAA TCATCNCACT 540
GCANCAAAAG CTGCCTGGCC TCANAAGCAT CCCGAGCTTG ACNGCGAAGG GATAGTCNTN 600
AACNCTNANC GCGTTNCGGC ATATATCAAT GTNAANAGTG GTGGCTGTGC TGCGTCCGTG 660
ACACTTNATG AACTGGCCGC GCTGGGAAGA TCTGTTCTCC GTCNAACTCA CCANANTCNA 720
ACCTAACCCC NTNCNCTTCC NGGGTTCTCC TTNATGCACT NTGCNCCTAT TTNTTTCCCA 780
ANGC 784

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 817 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

CGGCACGAGA TATGGAGGTA TGATCGGGAG CTACTGGGAG CTCCGCTTTG GTGAACAACA 60
CGACGGCAAG AAGGGCTATG GATTCAAGGA GTGAAGGCCA TGGTACCGCA NAGGCGGGTC 120
TTCCGGGCGT GCACCGAATT TTGCATCGGA TGAAAACCTT GGTCATCAGC ATATGGGGGC 180
TGGGTTCCAC CAAGGGAAAA GTTCGAATGC AAGTACCAGT GAGTCCCATG AGAGGGACTT 240
GATCATGCAG AGGTATGATC GAAGCAGCTG GAGANTTGGA CTGCTCCANA GCTCATATTC 300

GCTTAAGGGA GCCCGACAAG TCAGAGGACA AGGTCGAGTA AGCGAACGTT GCTACCCAAA 360

ATCAAGCATC AGTTANAATG GAGGTGGACT CANAGGAGTG CCACGGAAGA CATCTCTACT 420

GATTGTGAAG GAAAGGGATA CAGAGGCGAA NCGACGGATA NTANGGCCAT GGGCATGGCA 480

GCGCCATGGT ACCGCANANG CGGGACTTCC GTGCAAGTCA TTGATCCCTT GCTCTCACGG 540

AGGGANANCG CTTGGTCCTG AAAGGGGCCN AAGAAGTGGA CATGCANANG CAATCTCCAA 600

TTACCGAAAC ANGGCTGAAG GGCANAAGCC NANAAACTTC CTNAGAACGG TGTCAACAAT 660

TTCTCATCNA NATANCCGTA ATTAANGACT TCCGGTCATG CNANAATNCC CNACCNANGA 720

ACCAANCAGG CNTACTTGTG CTGTNCTTTG CTACCCNNTG AATNGCGCCN GGTTNATNGA 780

AAAAACGTCC TTCCCCAAGC AACCCTCTNT CAAAAAN 817

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 837 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TTTTTTTTTT TTTTTTTTGG GTATCAGGCA AAGATGGATA CTTCCAGGTT TGCTATTTAA 60

GAACCATAGT CAGTCTTATG AGGAGAGACC ATACGTAATA CAATCTTTAA GATGACAAAA 120

TCCATTCCTA CCAATACAAT GACCAAGCGA AAGGTACAAG GATAACGGGC AAAAGACTAA 180

ATTGCAACTA TATAAAATTC TGCTGCATTG TAGTAAATTC AACTGTGACG ACACGCCACC 240

AGGATGAAGT CTATCTATAA ACCCACTTAT TGCTAGATGG ACGGTGTAAC AGAGCTAAAA 300

CAGCAAAGTA GAATAAAAGA AACTGACAAC GCTTCCGCAT GCGCTCCACA TATGGAGCCA 360

GGCGGAGGTT GGGCAATTGG AGGAAATGAC NTTTCTGACG GTGTAACATA AAANAAATTT 420

GTAACACCGT CAAGTACGAT TTCCCATCCT TCGGGTTGTG GCGTTCTGCT ACTTGGCATT 480

ACGTTAACAT CGAGTGCCGA CTTGGCAAGA CAGGACCCCA GCATCAGAAG TCAGTGTGTC 540

AACCAAGGAA GAAGGCTTGG CCCCAAAGCT GGAGGCCCGT GCGTAACTGG CTGAACCCCT 600

GCACCGGAAN GGGTGAAAAA AGCACCATTC AGAACAGGTC NCCTCCGACC TCCCAATTCC 660

AGTTCTTCCA CCNTGCTTTT GATCTGTGTC CACCTTTTTG TTACCTATTC CATCGAAGCN 720

TANGGATTTT TAAAAATCCC GAAGGAAAGG AANTTCCNAT AATTGGTGCN CCAAANAAGG 780

AAGATGGACN GAACTGTTGT TGGTTGCTCC TGTTCCTCCT TTGCAATGGA TTGGTCG 837

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 799 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GGCACGAGGC AGCTCAATCG ACCGACTCCT CCTCCTCCTC CTCCTCCTCC TCTTGTTCTT 60

CTCATTCTAA TATAATTATC GCTTTTGGTG TGTACATCTT CTATAATTTG AGAGGATGGA 120

GGCAGGATTG ATGGCGAAAC AAGCAGCAGC GGTTGCGAAG CCGAACGCGT TCCCCGCCCG 180

GAGCCTAGGG TTCGGGAGCT CGGTCAGGGG CGGATCCGGG ACCAGCAGGA TCGGGTTCGA 240

GGCGCCCGCG AGCGTGGCAT GGAGGAAGCG GTCGATTCAG GTGGCCCGCC AAGGAGCCAT 300

TCGGTCGGAG GTGGTCGTGG AANANAAAGC ATCNCCGCCC AAAAAGGATA AGGCCGGTCC 360

GGGTCGGCTC TACGTGGGTC TGCCCTTGGA CGTGGTCTCC GACGGCAACG TCNTCAACCA 420

CGGCAAGGCC ATCGCCGCCG GTCTCCGCGC CCTCCGCCCT CCTCGGCGTT GATGGANTCN 480

AACTCCCCCA TCTCCTGGGG CGTTGGCGAT GGACTCCGGC GAATGGTCCT CCTACCTCCC 540

CCGTCNCCGC CATGGCGCGC GACNCCCGGC CTTCGCCTCC GCGTCTCCCT CCACCTCCAC 600

TGCCANCGCC GCCCTCGCCT CCCCCTCCCC NAATCGGTCG AATCCNCCGC CGCTAACAAA 660

CCCCGAAATC CTATTCNCTG AACGCNCCGG CCGCCNCCNG TTGCCCAAAN TNGCCTTNTT 720

CCTTTCCNCT TTGTTTNAAA AAAAACTCCC CNTTGTTCCT TCCAANCGGG NAGGAACCCC 780

CNAATGGAAA CCTTNCAAA 799

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 786 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GGCACGAGGA AACGTCTCTC CCTCTCTCCA CTTCTCACAC CCCCGCCCCC GACTCAGCGA 60

ATCGACATTC TTGGCGTGTC AAGGAAACCT TTCTTTTATT TGCGAAGGAA CATGAGCAAT 120

ACTGTTGGAC ACACCTTACC CCAGCAAGCT CTTTACCGGC CTTCTATCAA AGAAAATCAA 180

AGTAAAGCTC ATCAAGGAGT TTCTGCAAAC TTCTTGTGTG GAGTTCCATT AGGATCTAAG 240

GTGGAAAATG CAGTGTCATA CAGCTCTAGG TCACTGCTTT CAACCGGATC CCTGGGAAAG 300

AAACTCATCA AAGGAATC. ACCAAAGCAA AATCCAAGCA TAGTCACTAT GACCCCTCGT 360

GCTGTGTTGG CTGCANATCC TGCTTCAGAG CTAAGGAGAA AATTCAAGCT TGACACAAAT 420

TCTGAATTGG AGGTTGTTGT TCATGTCCCT ACTTCGGGGT CTCCTGTNCA GATTGAATTT 480

CAAGTNACTA ACAGCAGTGG CTACTTGGTG CTTCNTTGGG GTGCAATTCA TAATANAAGG 540

AATAACTGGT CACTTCCTTC TCGTCATCCT GATGGAACAA AAGTTTNCCN AAACCCGAAC 600

TCTCANGANA CCTTTTAAAA AATCTGGTTC CCCATCNTCC GTNAAAATGG AGATTGATGA 660

TCCTGAAATA CCAGCAGTNG AATTTCTCCT TANTTTTGNA ACAAATNCTC AAAAAAACCN 720

AAATTGGGTT TTTAAAACNA TTAATGGGTC CCNAAATTTC CNTGTTCCNN TTTTTTTANA 780

AACAAG 786

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 804 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

GGCACGAGAG ATAGCTGAAG TGACGTGAGG TGACTTCGAT TAGATCGAGA GAAATTTCTT 60

TGTGATTTTT GTGGACAATT CTCAATGGCT GCTGTAACAA ANTCACAATT CATCTCGAAA 120

GGCTCATGCG CTGGCTATGG GGGTGTCGTC GACTCGGAGC CAAGGACCTT CCTAAACAGA 180

AGGGTTCTAC ACTTGAGGAA CCAAACCACC GCTTACGAAG GATTGAGATC TCGAAATGTG 240

GTTGATTTGA TTCAGATGCC GTCTAATGCC AAGGTGATTT CAAGGAAAAC TGTGAGGGGA 300

ACTCAGAATC CTAGTCGTAN ACCTTGGGCT GTTGTCATTT GTGGAAAAGG GATGAACATA 360

GTCTTTGTCG GCGCTGANAT GGCTCCCTGG AGTAAAACCG GANGGACTCG GTGATGTTCT 420

TGGAGGACTG CCACCGGCCA TGGCTGCAAA TGGACACAGA NTGATGACTA TAGCTCCACC 480

CTATGATCAG TACAAGGATG GGTGGGATAC AAATGTCCTG GCTGAATTAA AAGTTGGAAA 540

TGAAATTGAA ANAATCCGCT TTCTTCCACT GCTATAAAAA AAGAATTGAC AGGGTTTTCA 600

TTGATCACCT TTGTTTCTTG AAAANGTGTT GGGAAAAACT GGAAGAATGA AATTTTGGTC 660

CTNTCCCCGG AACTGATTTT NAAAAACANC CCCTAAANTT TANCCTTTTN TNCCCNGCCN 720

CTTTTGGAAA CTCCCNGGAT NCTGGTTTTT TNCCACCCCC NAAAANTTTC CTNGAACCTN 780

TGGGGGAAAN TTTTTTTTTT TTTT 804

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GGCACGAGAG ATAGCTGAAG TGACGTGAGT GGACAATTCT CAATGGCTGC TGTAACAAAG 60
TCACAATTCA TCTCGAAAGG CTCATGCGCT GGCTATGGGG GTGTCGTCGA CTCTGAGCCA 120
AGGACCTTCC TAAACAGAAG GGTTCTACAC TTGAGGAACC AAACCACCGC TTACGAAGGA 180
TTGAGATCTC GAAATGTGGT TGATTTGATT CAGATGCCGT CTAATGCCAA GGTGATTTCG 240
AGGAAAACTG TGAGGGGAAC TCAGAATCCT AGTCGTANAC CTTGGGCTGT TGTCATTTGT 300
GGAAAAGGGA TGAACATAGT CTTTGTCGGC GCTGANATGG CTCCCTGGAG TAAAACCGGA 360
GGACTCGGTG ATGTTCTTGG AGGACTGCCA CCGGCCATGG CTGCAAATGG ACACAGAAGT 420
GATGACTATA GCTCCACGCT ATGATCAGTA CAAGGATGGG TGGGATACAA ATGTCCTGGC 480
TGANTTAAAA GTTGGAAATG AAATTGAAAG AATCCGCTTC TTCCACTGCT ATNAAANAAG 540
AATTGACAGG GTTTTCATTG ATCATCCTTT GTTTTCTTGA AAANGTGTTG GGAAAAACTG 600
GANGAATGAT ATNTGGTCCT GTCCCNGGAA CGGATTATTN AAAACCACCC NCTTAANATT 660
TACCCTTTTG TGCCCANGCA NCNTTTGGAA NCTCCCAAGG ATTCTGGATN TTTAACNACN 720
NCCNAATACT TTTCCTGGAA CCATTTNGGG GANAANNTTG TTNTTTGTTG CNAATTAATT 780
GGCNCCCTGG TCCTCCTNCC TGCTACTTAA AAATTTTNTT TCNTNT 826

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 813 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

GGCACGAGCT GAGGGAGTGA GGGAAAGAGA TAGCTGAAGT GACGTGAGGT GACTTCGATT 60
AGATCGAGAG AAATTTCTTT GTGATTTTTG TGGACAATTC TCAATGGCTG CTGTAACAAA 120
GTCACAATTC ATCTCGAAAG GCTCATGCGC TGGCTATGGG GGTGTCGTCG ACTCGGAGCC 180
AAGGACCTTC CTAAACAGAA GGGTTCTACA CTTGAGGAAC CAAACCACCG CTTACGAAGG 240
ATTGAGATCT CGAAATGTGG TTGATTTGAT TCAGATGCCG TCTAATGCCA AGGTGATTTC 300
AAGGGAAAAC TGTGAGGGGA ACTCAGAATC CTAGTCGTAG ACCTTGGGCT GTTGTCATTT 360
GTGGAAAAGG GATGAACATA GTCTTTGTCG GCGCTGANAT GGCTCCCTGG GAGTAAAACC 420
GGAGGACTCG GTGATGTTCT TGGAGGACTG CCACCGGGCC ATGGCTGCAA ATGGACACAG 480
AAGTGATGAC TATAGCTCCA CGCTATGATC AGTACAAGGA TGGGTGGGAT NCAAATGTCC 540

TGGCTGAATT AAAAGTTGGG AAATGAANTT GAAAGAATCC GCTTCTTCCA CTGCTATAAA 600

ANAAGAATTG ACAGGGTTTT CATTGATCAC CTTTGTTCTT GAAAAGGTGT GGGGAAAAAC 660

TGGAAGAATG ATATTTGGTC CTGTCCCNGG ACTGATTTNA AAACACCACC TAAAATTACC 720

TTTTGTNCCN GCNNCTTTGG AACCNCCCNG GATCTNGATN TTANCACCCC CAANTCTTAT 780

CCTGGAACTT TTGGGGNAAA NTTTGTNTTT GTT 813

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 805 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GGCACGAGAA GAGATAGCTG AAGTGACGTG AGTGGACAAT TCTCAATGGC TGCTGTAACA 60

AAGTCACAAT TCATCTCGAA AGGCTCATGC GCTGGCTATG GGGGTGTCGT CGACTCGGAG 120

CCAAGGACCT TCCTAAACAG AAGGGTTCTA CACTTGAGGA ACCANACCAC CGCTTACGAA 180

GGATTGANAT CTCGAAATGT GGTTGATTTG ATTCAGATGC CGTCTAATGC CAAGGTGATT 240

TCAAGGAAAA CTGTGAGGGG AACTCACAAT CCTAGTCGTA NACCTTGGGC TGTTGTCATT 300

TGTGGAAAAG GGATGAACAT AGTCTTTGTC GGCGCTGAGA TGGCTCCCTG GANTAAAACC 360

GGAGGACTCG GTGATGTTCT TGGAGGACTG CCACCGGCCA TGGCTGCAAA TGGACACACA 420

GTGATGACTA TAGCTCCACG CTATGATCAG TACAAGGATG GGTGGGATAC AAATGTCCTG 480

GCTGANTTAA AANTTGGAAA TGAAATTGAA AAGANTCCGC TTCTTCCACT GCTATAAAAN 540

AAGAATTGAC AGGGTTTTCA TTGATCATCC TTTGTTTCTT GAAAAAGTGT GGGGAAAAAC 600

TGGGAAGAAT GATATNTGGT CCTGTCCCNG GAACTGATTA TAAAACACCA GCTAANATTA 660

CCTTTTGTTG CCAGCAACTT TGGAACCCCN AGGATTCTGG ATNTTACAAC ACNAATACTA 720

TTCTGGAACA TTTGGGGAAA AATTGTTTTT GTTNCCAATG ANTGGCNCAC TGGTCCCNTC 780

CCTNCCTACT TAAAAANTTT TTTCC 805

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 790 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GGCACGAGAA GAGATAGCTG AAGTGACGTG AGTGGACAAT TCTCAATGGC TGCTGTAACA 60

AAGTCACAAT TCATCTCGAA AGGCTCATGC GCTGGCTATG GGGGTGTCGT CGACTCTGAG 120

CCAAGGACCT TCCTAAACAG AAGGGTTCTA CACTTGAGGA ACCAAACCAC CGCTTACGAA 180

GGATTGAGAT CTCGAAATGT GGTTGATTTG ATTCAGATGC CGTCTAATGC CAAGGTGATT 240

TCGAGGAAAA CTGTGAGGGG AACTCAGAAT CCTAGTCGTA GACCTTGGGC TGTTGTCATT 300

TGTGGAAAAG GGATGAACAT AGTCTTTGTC GGCGCTGANA TGGCTCCCTG GAGTAAAACC 360

GGAGGACTCG GTGATGTTCT TGGAGGACTG CCACCGGCCA TGGCTGCAAA TGGACACAGA 420

GTGATGACTA TAGCTCCACG CTATGATCAG TACAAGGATG GGTGGGATAC AAATGTCCTG 480

GCTGAGTTAA AAGTTGGAAA TGAAATTGAA AGANTCCGCT TCTTCCACTG CTATAAAAGA 540

AGANTTGACA GGGTTTTCAT TGATCATCCT TTGTTTCTTG ANAAGGTGTG GGGAAAAACT 600

GGAAGAATGA TATATGGTCC CTGTCNCAGG AACNGATTAT GAANACAACC AGCTAAGATT 660

AACCTTTTGT TGCCAGCACT TTGGGAACCN CAAGGATCCT GGATCTTAAC AACNCAANTC 720

TATTCTGGAC CATATGGGGA CAAATTGTTT TGTTGCAAAT GATGGCACCT GGTCCNNTCC 780

ATGCTACTTA 790

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 813 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

TTTTTTTTTT TTTTTTTTTG GAGCATAATA GCAATTTATT CAGGAGGATC AAACTCAAAC 60

ACTATAACAT AGACAGTAGT CACTTTCAGG GAGTGGCCAC ATTTTCCTTT GCAAGAGGAG 120

CTATTTCATC AGCATCGATG CCGGCTTCAC TACCAGCAGC TCCTAAGCTT AGGANAAATT 180

GCTCCCACTT CTTAGCAGGT CCCTTCCAGG AGAGGTCTTG AGTCATGCAG TTCTGTATCA 240

TCTCAGCAAA TGCAGGTGTG CCGTAAACTT TAAGGGCCCT TTTCACTGTC TGAATGACTT 300

TTTGTACATC ATCTTTATCG ACAACATCAC AATCAGGATT GAAGGGACCC ATATGAAACC 360

CTGTGATGCC TTCTATGACA GTGTCAGCAA GTCCACCAGT TGTTGCGCAC ATGGGGGGAA 420

TTCCATATCG CATGCCCTGA AAGCTGGATA AGGCCACAAG GTTCGAATCT GCTGGTAAGA 480

NCAAGAAGAT CTGCTCCAGC CATGATTTCA TGANCCAAAG GTGCATTAAA CTTCATATGT 540

GCTCTCACTT TATTGGGAAA CATATCTTCA AGTTGTGCAA GCTGACGCTC CAACANCTTC 600

TCCCANTACC AAGCACTATC ACTTGAACAT TTTCATCAAT GAATTCAGGA ATAACTGCNG 660

CGAAAATATC CGAACCTTTC TGCTCTCTAA TCTCCCTATA AAGGNTATAA CAGGGATTTC 720

CNGTCAACAG GTTAACCAAA TTCAACTTGT TAGGNTTCCC TTAATCCAAA GGTTTGCACC 780

CNNCCCATTT GTTGCTCNTA ATTGANAAAA ATT 813

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 808 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GGCACGAGCG AGTTTTTTTT TTTTTTTTTT GCTGTGATGA TATTATGCAT CTTATTAGTT 60

GGTTGCACCA CTTCTATTAC ATCACTCAAC AGTATTAGCC CAAGANAAGG CTAATACCTT 120

CNCATCACTC TTGACATCTT ATTTGTATTG TAGGANACTA GTATATATAT CTATATGCGT 180

GGTTGCCTGC ACNAGGGCGG CTTATTAGTG GCGTCAGTGA TCTCAAGGGC AGAANACAAC 240

CCTGTANTTG GTGCCGCCGG GGCAGGTGAA GGTGCTCGTC TGATCGTCCT TGGGATANCT 300

GTAGGCGTCG GGGCAGTTTC TCTTGAANAA CCGGGAGTAT TCGGTCGGGC TGCAGCTGCC 360

GGAGTTGCAA CAGTACTGGT CCGTCTTGAA CACGGTGCAG GGGTTGTTGC ANCCGCCCGG 420

CGCCTTCANC GCCCCGGGGC ACTGCCCGTT GATNTCCGCC GCGCACCGGA TGCCGCGGCA 480

NCCGCCTGAC NTGGGGCTNA ATCCCATTGG CACGTTGAAA CCGTCNACCA AGGGAAATTT 540

CAAAAAATCC AAGTTGTTGA ACTGGTTGAA CGCCAACTCC NCCAGGGTNT TGGGCCGGTT 600

GCCNTACCCC GTGCATNACA ACACCCCGCC GCANTCCCCT TCTGGCACCG CCGCNTCCGC 660

TCCCCTCAAA AGAACACCCG TGCGGCCCAA AATCCGGNCC CCCGGTGGTT CCCCCTTTCN 720

CTTTAANGGT CCCCAATGCC CCTGNTTTAA CTGNCTCCCC CCCANGCNCG GCCCCGGCCC 780

ACNCTTTNTT AAAACATCNG TNCCNAAT 808

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 809 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGCACGAGTG TGCCTAACAG AGAAAGAGAG ACCGATAGCC TCCTCATTCA CTATGGCGAT 60

CCGATCGCCA GCTTCGCTGC TGTTATTTGC GTTTCTGATG CTTGCGCTCA CAGGAAGACT 120

GCAGGCCGGG CGCAGCTCGT GCATTGGCGT CTACTGGGGA CAAAACACAG ACGAGGGAAG 180

CTTAGCAGAT GCTTGTGCCA CAGGCAACTA CGAATACGTG AACATCGCCA CCCTTTTCAA 240

GTTTGGCATG GGCCAAACTC CANAGATCAA CCTCGCCGGC CACTGTGACC CTCGGAACAA 300

CGGCTGCGCG CGCTTAAGCA GAGAAATCCA GTCCTGCCAG GAGCGTGGAG TCACGGTGAT 360

GCTCTCCATC GGAGGTGGCG GGTCTTATGG CCTGAGTTCC ACCGAAGACG CCAAGGACGT 420

GGCGTCATAC CTCTGGCACA GTTTCTTGGG TGGTTCTGCT GCTCGCTACT CTCGACCCCT 480

CGGGGATGCG GTTCTGGATG GCATANACTT CAACATCNCC GGAGGGAGCA CAGAACACTA 540

TGATGAACTT GCCGCTTTCC TCAAGGGCTA CNACGAACAG GAAGCCGGAA CGAAAAAANT 600

TTTACTTGAA TGCTGCTCCC NCANTGTCCT TTCCCGGATT ACTGGCTTGG CACCCACTCA 660

NAAAANATCT CTTCCNACTT CCNTGTGGGT TGCANTTCCT CCAANAACCC TTCCTTGCCN 720

TTTCTCCCCA AAACCTATCC ATCTTGCAAT TCCTTTCACA AATTGGGTCN TNTCCNTCCC 780

NGCCCCNAAA ACTTTTTCCC TNGGGCTCC 809

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 809 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

GGCACGAGCC ACAAGCTTGC CTTTGGTTGT GCCTAACAGA GAGAGAGAGA GAGACAGACC 60

GATAGCCTCC TCATTCACTA TGGCGATCCG ATCGCCAGCT TCGCTGCTGT TATTTGCGTT 120

TCTGATGCTT GCGCTCACAG GAAGACTGCA GGCCCGGCGC AACTCATGCA TTGGCGTCTA 180

CTGGGGACAA AAGACAGACG AGGGAAGCTT AGCAGATGCT TGTGCCACAG GCAACTACGA 240

ATACGTGAAC ATCGCCACCC TTTTCAAGTT TGGCATGGGC CAAACTCCAG AGATCAACCT 300

CGCTAGCCAC TGTGACCCTC AGAACAACGG CTGCGCGCGC TTAAGCAGCG AAATCCAGTC 360

CTGCCAGGAG CGTGGAGTCA AGGTGATGCT CTCCATCGGA GGTGGCGGGT CTTATGGCCT 420

GAGTTCCACC GAAGACGCCA AGGACGTGGC GTCATACCTC TGGCACAGTT TCTTGGGTGG 480

TTCTGCTGCT CGCTACTCTC GACCCCTCGG GGATGCGGTT CTGGATGGCA TAAACTTCAA 540

CATCNCCGGA GGGAGCACAG AACACTATGA TGAACTTGCC GCTTTCCTCA AGGGCTACAA 600

CGANCAGGAA GCCGGAACGA AAAAAGTTCA CTTGAATGCT GCTCCCCANT GTCTTTCCCG 660

GATTACTGGC TTGGCAACGC NCTCCAAAAC AAATCTCTTC CACTTCCTGT GGGTGCANTC 720

CTCCACAAAC CTTCNTGCAT TCTCCCCAAA CCTATCAATC TTGCNAAATG CGTTCAACAA 780

TTNGGGTCTT TTCATCCCCG CCCAAAACT 809

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 785 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GGCACGAGGA GAGACCGATA GCCTCCTCAT TCACTATGGC GATCCGATCG CCAGCTTCGC 60

TGCTGTTATT TGCGTTTCTG ATGCTTGCGC TCACAGGAAG ACTGCAGGCC GGGCGCAGCT 120

CGTGCATTGG CGTCTACTGG GGACAAAACA CAGACGAGGG AAGCTTAGCA GATGCTTGTG 180

CCACAGGCAA CTACGAATAC GTGAACATCG CCACCCTTTT CAAGTTTGGC ATGGGCCAAA 240

CTCCAGAGAT CAACCTCGCC GGCCACTGTG ACCCTCGGAA CAACGGCTGC GCGCGCTTAA 300

GCAGAGAAAT CCAGTCCTGC CAGGAGCGTG GAGTCACGGT GATGCTCTCC ATCGGAGGTG 360

GCGGGTCTTA TGGCCTGAGT TCCACCGAAG ACGCCAAGGA CGTGGCGTCA TACCTCTGGC 420

ACAGTTTCTT GGGTGGTTCT GCTGCTCGCT ACTCTCGACC CCTCGGGGAT GCGGTTCTGG 480

ATGGCATANA CTTCAACATC GCCGGAGGGA GCACAGAACA CTATGATGAA CTTGCCGCTT 540

TCCTCAAGGC CTACAACGAG CAGGAAGCCG GAACGAAAAA AGTTTACTTG AATTGCTGCT 600

CCGCANTATC CTTTCCNGAT TACTGGCTTG GCAACNCNCT CCAAAAAANA TCTCTTCCAC 660

TTCCTGTTGG GTGCAGTTCT TCCAANAACC CNTTCNTGCC ATTTCTCCCC AAAACGCTTT 720

CCATCTTTGC AAATGCCTTT CAACAATTGG GGTCTTGTTC CNNCCCTGCC CCAAAAACTG 780

TTCCT 785

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 813 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

GGCACGAGCG ATAGCCTCCT CATTCACTAT GGCGATCCGA TCGCCAACTT CGCTGCTGTT 60

ATTTGCGTTC CTGATGCTTG CGCTCACGGG AAGACTGCAG GCCCGGCCCA GCTCATGCAT 120

TGGCGTCTAC TGGGGACAAA ACACCGACGA GGGAAGCTTA GCAGATGCTT GTGCCACAGG 180

CAACTACGAT TACGTGAACA TCGCCACCCT TTTCAAGTTT GGCATGGGCC AAACTCCAGA 240

GATCAACCTC GCCGGCCACT GTGACCCTCG GAACAACGGC TGCGCGCGCT TGAGCAGCGA 300

AATCCAGTCC TGCCAGGAGC GTGGCGTCAA GGTGATGCTC TCCATCGGAG GTGGCGGGTC 360

TTATGGCCTG AGTTCCACCG AAGACGCCAA GGGAAGTAGC GTCATACCTC TGGCACAGTT 420

TCTTGGGTGG TTCTGCTGCT CGCTACTCGA GACCCCTCGG GGATGCGGAA CTGGATGGCA 480

TANACTTCAA CATCGCCGGA GGGAGAACAG AACACTATGA TGAACTTGCC GCTTTCCTCA 540

AGGCCTACAA CGANCAGGAA GCCGGAACNA AAAAAGTTCA CTTGAATTGC TGCTCCGCAG 600

TGTCCTTTCC CGGATTACTG GCTTGGCAAC GCACTCAGAA CANATCTCTT CNACTTCCTG 660

TGGGTGCAAT TTCCTCCACA ANCCTTCCNT GCCATTTCTC CCAAAAAGCT ATCNATCTTG 720

CAAATGCGTT CNACAATTGG GTCTTTTCCA NCCTGCNCAA AACTGTTCCT TGGGCTCCCG 780

CTGCCCCTGA AGGTGCNCCA ATTGGTGGCT NCT 813

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GGCACTCAGG AACTCCAACA TCCAAGTCCT GTTGGATGTC CCCCGATCCG ACGTGCAGTC 60

ACTGGCCTCC AATCCTTCGG CCGCCGGCGA CTGGATCCGG AGGAACGTCG TCGCCTACTG 120

GCCCAGCGTC TCCTTTCGAT ACATAGCTGT CGGAAACGAG CTGATCCCCG GATCGGATCT 180

GGCGCAGTAC ATCCTCCCCG CCATGCGCAA CATCTACAAT GCTTTGTCCT CGGCTGGCCT 240

GCAAAACCAG ATCAAGGTCT CGACCGCGGT CGACACGGGC GTCCTCGGCA CGTCCTACCC 300

TCCCTCCGCC GGCGCCTTCT CCTCCGCCGC CCAGGCGTAC CTGAGCCCCA TCGTGCAGTT 360

CTTGGCGAGT AACGGAGCGC CGCTCCTGGT CAATGTGTAC CCTTATTTTA GCTACACCGG 420

CAACCCGGGA CAGATCTCGC TGCCCTACGC CCTGTTCACG GCCTCCGGCG TCGTCGTGCA 480

GGATGGGCGA TTCANCTATC AGAACCTGTT CGACGCCATC GTCGACGCGG TCTTCGCGGC 540

GCCTGGAAAA AATGGGAAGG GCGAACGTGG CGGTGGTGGT GTCCGAAAAC GGGTGGCCGT 600

CCGCGGGCGG AAGAACCCNA AACNAACACC ANCAACNCCG CCGGAANTTT CAACCANAAC 660

TTGATCAGGC ATGTTNGGCG GAAGAACCCC AAGGAAAACC AGGGAAGGAA ATCAAGGCTT 720

CNTNTTCCAA AANTTTCCAC CAAAAACCNA AAGGTGGANG GATCCAACAA AACTTTGGCC 780

TGTTTTATCC CAANNAACAN CCCNTCTTAC CNAATAACT 819

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 794 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

GGCACGAGGG ATTATAAAAA GAAACTCGCA CTCAGCCAGA TTGACTCAAG CATGAAGGTT 60
GCATCTTTCG AATGTTCCTT TTTTTTCCAA CATCTTTTGA ATGTTACATG ACAATCATGA 120
CGCCGTGCAT ACAATGATAC CTCTGATAGG GTTGAATGCA CAAACCACTC ATCGTGCTAT 180
ATTGCAAGTG CTTATGTTTG TATTCATTTT CTTATAATTT CAATGTGAGA GTTACCTTAG 240
GTTCATATTA NATTTATATA ATATTGGGCA TAGATTTTTT TGTCATTGTT TGTGATCTGC 300
AATTTCATTA GGTCATCGAC CATATTATGG TAAATTTAAT TTACTAAATT ATATCTTGAG 360
TTTATTGCTT TGCATATTTT GTGCTGGAAA CCATGCCAAT CCAACTCCTT TGCAAAACTT 420
AAGATAATTA AAGGAGATAT TGAGGATGCC GACTGCTTTA GGTTATTTGC ATTANACAAT 480
AAACGCCCGT GAAATGGAAA TCATGCAAAG CTTTGCATGG AGAATATGTT NATAGAGATA 540
GACATGAAGA CATGAATATG CTTTCTTGAT GAACAACGAT GTTCACNTGT TTACTGCATG 600
CATGATACAT CCAATGTTCT AGGCTTGTTG GCAATCATTT TATTCNAAAA ATTGTCTGTT 660
TCTCTNCCNC CATAAGGTTA GCTTGTGGAA AATGTTCAAC TTTGGGCNCA NATGATCCGT 720
TTTAGCAAAA TCCCNCCATT CCTATTTTTT TCCGGAATCC NNTTGGNAAA ANATCCTNAC 780
ATACTATTTC CACA 794

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 798 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGCACGAGGC CCGTAGAGCG AGTGCTGAGA TGGCTTTGAG GGCCTTCTTC CCCCTCTGCA 60
TCGCTCTCGT GGTGACGCTC TCACCTCTGT GTGATGCCAC TTCGCCTTAC TACACCATCA 120
CACCGCCCAC CCCCGTGGCC AAGCCGCCTT CAGTTGAACC ACCACCCTAC CACGGCCCTC 180
CGACGACCCA CCCTAAGCCA CCGAGTCATG GTGGCCAACC TCCGTCCCAC CATCACCCAA 240

CACCAATCTA CGGTGCACCC CCTCCGCAAC ACCACCACCA CCACCAACAC CACCACCAAC 300

CTGCACCACC AACTCACGCA GAACACCCTC CGTACTACCA CATGCCTTCC CCGCCGCCGC 360

ATGGCCAGCA CCCGTCACCA CCGTCACATG ATTATCCCGT ACCTCCTGCT CACAAGCCCC 420

GAACTCCGCC GCCGGTTTAC AAGTCTCCAC CACCGACCCA CCGTCCTTAC CCTCCATCGA 480

CGCCACCCCA CCATCCGACG CACCCGCCTT CTCAGCCGAC GCCGTCATAC AAGGCCCCGC 540

CACCATACAA GAACATCCCT GANCATCTCC ACCGCCGCGT CACTATCATT CTCCGTCTTC 600

ACCACCANCA CAACCACCAT NCAAATAGTC TCGTTTGCAT CTCTCCGTTG AANATGAACC 660

AATGTCNTTT AATAACGATC AGGGTTTCAA ATAAAAACNA ATTTCCGCCA TTGTAATGCT 720

ATGGTTGTTC TCTCTGCTTC CCGGGGAAAG TTTCTTGGGT CATNTTAACC NCCTCCTAAT 780

GTTCNGCTCT TNNTANAA 798

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 824 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GGCACGAGCG CCCACCCCCG TGGCCAAGCC GCCTTCAGTT GAACCACCAC CCTACCACGG 60

CCCTCCGACG ACCCACCCTA AGCCACCGAG TCATGGTGGC CAACCTCCGT CCCACCATCA 120

CCCAACACCA ATCTACGGTG CACCCCCTCC GCAACACCAC CACCACCACC AACACCACCA 180

CCAACCTGCA CCACCAACTC ACGCAGAACA CCCTCCGTAC TACCACATGC CTTCCCCGCC 240

GCCGCATGGC CAGCACCCGT CACCACCGTC ACATGATTAT CCCGTACCTC CTGCTCACAA 300

GCCCCGAACT CCGCCGCCGG TTTACAAGTC TCCACCACCG ACCCACCGTC CTTACCCTCC 360

ATCGACGCCA CCCCACCATC CGACGCACCC GCCTTCTCAG CCGACGCCGT CATACAAGGC 420

CCCGCCANCA TNCNAGACCA TCCCTTGAGC ACTTCTCCAN CGNTTGCGTT TATTATCATT 480

CTCCGTCTTC ACCACCACCA CCACCACCAT ACAAATAGTC TCGTTTGCCA TCTCTCCGTT 540

GAAGATGACG CAGTGTCGTT TTAGTAGCGA TCAGGGTTAC CAATAAGAAC GATGTTGCCG 600

CCATTGTAAT GGCTATGGTT GTTCTCTCTG CTTTTCCGGG GGAAGGTTCT TTGGGTTCAT 660

GTTAAACCTC TCTCTTAAAT GTTCATGCAT CTTATTATAA ACNAAAATTG GCCATTTNNN 720

NNNTNTNNTN NNNNNTTNNN NNNNNAAAAC TCNAAAAATA TTTTTAAAAA CGGGCGGGGG 780

GCCCATCNAT TTTCCNNCCC GGGTNGGGGN TCCCAGNTTA TTNT 824

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 797 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GGCACGAGGG TTACGATCGT CATGTTGGGG GTGTTCAGCG GGGNAGGTGG TGGAGGTGCC 60

GGCGGAGCTG GTGGCCGCCG GCAGCAGGAC GCCGTCCCCT AAGACACGAG CGTCGGAGCT 120

GATCAACCGA TTCCTCGGGA GCTTCGCTCC CGCGGTGTCG ATCCAGATCG GGGACTTGGG 180

ACACCTCGCC TACTCCCACG CCAACCAGTC CCCCTTCGCT CCCAGGTTGT TTGCAGCGAA 240

GGACGANATT TACTGCCTCT TCAAGGGAGT GCTGACCAAC CTGGGCAGCT TGAGGCAGCA 300

GTATGGGCTT TCCAAGAGTG CCGACNAGGT GGTGCTGGTC ATCGAAGCCT ACAAGGCCCT 360

CCGTGACCGA GCTCCCTATC CTCCCAGCTT CATGCTCGCA CACCTTACTG GCAACTTCGC 420

CTTCGTGCTC TTCGACAAGT CCACATCATC CATCCTTGTT GCATCTGACC CANATGGAAN 480

ANTACCCTTG TTCTGGGGGA TCACTGCANA TGGATGCCTT GCCTTTGCTG ACNATCTANA 540

CTTGCTGAAG GGATCGTGCG GGAAGTCACT TGCACCATTC CCTGAAGGAT GTTACTATTC 600

CAATGCCTTG GGGGGCCTGA AAANCTATGA AAACCCCAAC ACAAGGTGAA CTGCTGTTTC 660

TTGAANATGA AGAANAATTN TTTGTGCCNC TTTCAAGGTG GAANGATCTG CCNTTCTTGC 720

GGNAACCCCC TAATCAAGGA ACATCTTCCA ATGTTTGGGG CNAATGATCC TCTTAAAATC 780

CTAAAATTCT TGGAATT 797

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 804 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

GGCACGAGCT TCCACACAGG TGAGGGTAAG TCGGTTACGA TCGTCATGTT GGGGGTGTTC 60

AGCGGGGAGG TGGTGGAGGT GCCGGCGGAG CTGGTGGCCG CCGGCAGCAG GACGCCGTCC 120

CCTAAGACAC GGGCGTCGGA GCTGATCAAC CGATTCCTCG GGAGCTTCGC TCCCGCGGTG 180

TCGATCCAGA TCGGGGACTT GGGACACCTC GCCTACTCCC ACGCCAACCA GTCCCCCTTC 240

GCTCCCAGGT TGTTTGCAGC GAAGGACGAN ATTTACTGCC TCTTCAAGGG AGTGCTGACC 300

AACCTGGGCA GCTTGAGGCA GCAGTATGGG CTTTCCAAGA GTGCCGACNA GGTGGTGCTG 360

GTCATCGAAG CCTACAAGGC CCTCCGTGAC CGANCTCCCT ATCCTCCCAG CTTCATGCTC 420

GCACACCTTA TTGGCAACTT CGCCTTCGTG CTCTTCGACA AGTCCACATC ATCCATCCTT 480

GTTTGCATCT GACCCANATG GAAAAATGCC CTTGTTCTGG GGGATCACTG CANATGGATG 540

CCTTGCCTTT GCTGACNATC TANACTTGCT GAAGGGATCG TGCGGGAANT CACTTGCACA 600

TTCCCTGAAN GATGTTACTA TTCCAATGCC TTGGGGGGGC TGAAAANCTA TGAAAACCCA 660

ANCACAAGGT GACTGCTGTC TTGAANATAA AGAAAAATTT TTTGTGCCCC TTTCAAGGTT 720

GAANGATCTG CATTCTTGCG GCACCCCCTN ATCNAGGAAC NTCNTNCCAA TGTTGGGGCA 780

AATATCCTCT TTAAAANCAT AAAA 804

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 803 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-D64

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GGCACGAGGG ATTATAAAAA GAAACTCGCA CTCAGCCAGA TTGACTCAAG CATGAAGGTT 60

GCATCTTTCG AATGTTCCTT TTTTTTCCAA CATCTTTTGA ATGTTACATG ACAATCATGA 120

CGCCGTGCAT ACAATGATAC CTCTGATAGG GTTGAATGCA CAAACCACTC ATCGTGCTAT 180

ATTGCAAGTG CTTATGTTTG TATTCATTTT CTTATAATTT CAATGTGAGA GTTACCTTAG 240

GTTCATATTA GATTTATATA ATATTGGGCA TAGATTTTTT TGTCATTGTT TGTGATCTGC 300

AATTTCATTA GGTCATCGAC CATATTATGG TAAATTTAAT TTACTAAATT ATATCTTGAG 360

TTTATTGCTT TGCATATTTT GTGCTGGAAA CCATGCCAAT CCAACTCCTT TGCAAAACTT 420

AAGATAATTA AAGGAGATAT TGAGGATGCC GACTGCTTTA GGTTATTTGC ATTANACAAT 480

AAACGCCCGT GAAATGGAAA TCATGCNAAG CTTTGCATGG AGAATATGTT NATAGANATA 540

GACATGAAGA CATGAATATG CTTTCTTGAT GAACAACGAA GTTCACNTGT TTACTGCATG 600

CATGATACAT CCAATGTTCT AGGCTTGTTA GGCAACCTTT ATCCAAAAAA TTGTCTGTAC 660

TCTCCCCCAT AAGGTAAGCC TGTGGAAAAT GTTCACTTTG GGCCNNATGA TCAGTTTANC 720

CGAAAATCCC CCTTCNTTAT TTGTTTTCTG AAACNCNTTG GAAANANATT CCTTACATAC 780

CTTTTTCACN NANATNTTGA ACC 803

CLAIMS

1. A method of modulating the ripening or tissue senescence process in plants of the genus *Musa* comprising inserting into plant material at least one polynucleotide sequence selected from the sequences depicted as SEQ ID Nos 1 -57, regenerating said plant material and selecting from the transformed regenerants, plants with modulated ripening or tissue senescence characteristics.

2. A method according to claim 1 wherein the polynucleotide is obtained from the cDNA library having the NCIMB Accession Number 40814.

3. A method of modulating the ripening or tissue senescence process in plants of the genus *Musa* comprising inserting into plant material at least one polynucleotide sequence or a fragment thereof, obtainable by hybridisation, from the cDNA library having the NCIMB Accession Number 40814, by the use of at least one of the sequences depicted as SEQ ID Nos 1-57 as oligonucleotide probes, said hybridisation being conducted at a temperature from 60°C to 65°C in 0.3 strength citrate buffered saline containing 0.1% SDS followed by rinsing at the same temperature with 0.3 strength citrate buffered saline containing 0.1% SDS, regenerating said plant material and selecting from the transformed regenerants, plants with modulated ripening or tissue senescence characteristics.

4. A method according to claim 1 or 2 or 3, characterised in that the said polynucleotide modulates the production of pectate lyase.

5. A method according to claim 4 in which the polynucleotide sequence comprises at least one of the sequences depicted in the sequence listings as SEQ ID Nos. 13-18.

6. A method according to any preceding claim wherein the plant material is transformed using the *Agrobacterium*, microparticle bombardment, fibre mediated or direct insertion method.

7. Plants, their progeny and seed and material obtained from said plants, produced according to a method as claimed in claims 1 to 6.

8. A vector functional in plants comprising a promoter region which is operable in plant cells, a polynucleotide sequence defined in claims 1 to 3 and a transcription termination sequence.

9. A vector according to claim 8 wherein the promoter is constitutive, developmentally regulated or switchable.

10. A vector according to claim 9 wherein the promoter is tissue specific or organ specific.

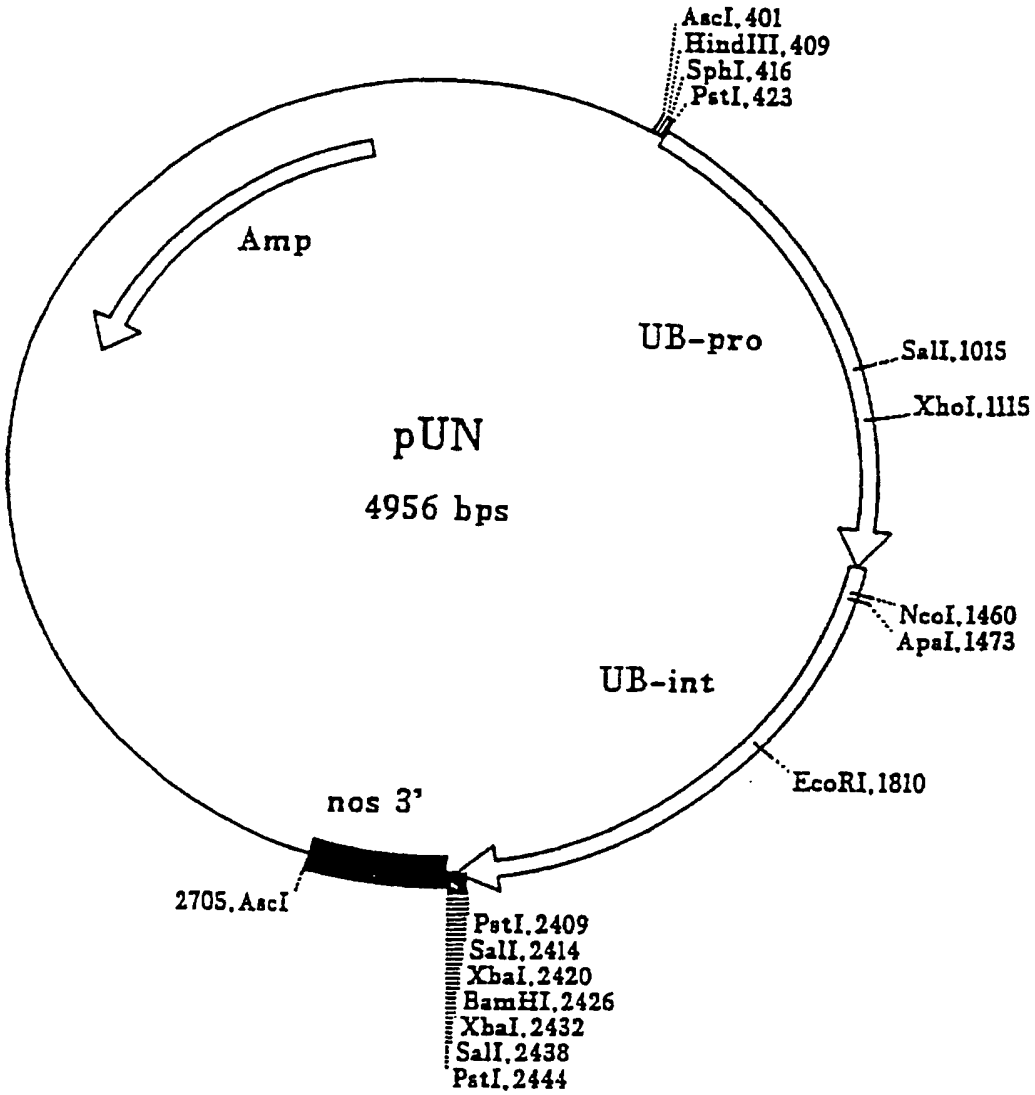
11. A genetically modified banana produced via the method according to claims 1 to 6 having altered fruit characteristics when compared with a banana which is not transformed with at least one of the polynucleotide sequences described in claims 1 to 3.

12. A method of controlling plant pathogens comprising the application of an anti-pathogenic agent to plants, characterised in that plants to which the said agent is applied are plants according to claim 7.

13. A polynucleotide associated with fruit ripening selected from SEQ ID Nos. 1-57.

14. A fruit of a plant of the genus *Musa* having a retarded ripening phenotype generated by inserting into the genome of the said plant at least one of the polynucleotide(s) as claimed in claim 13.

15. A method, polynucleotide, plant, its progeny, seed and material obtained from said plants and a banana substantially as hereinbefore described with reference to the accompanying drawings and figures.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ApaI, 1473
UB-int
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nos 3'
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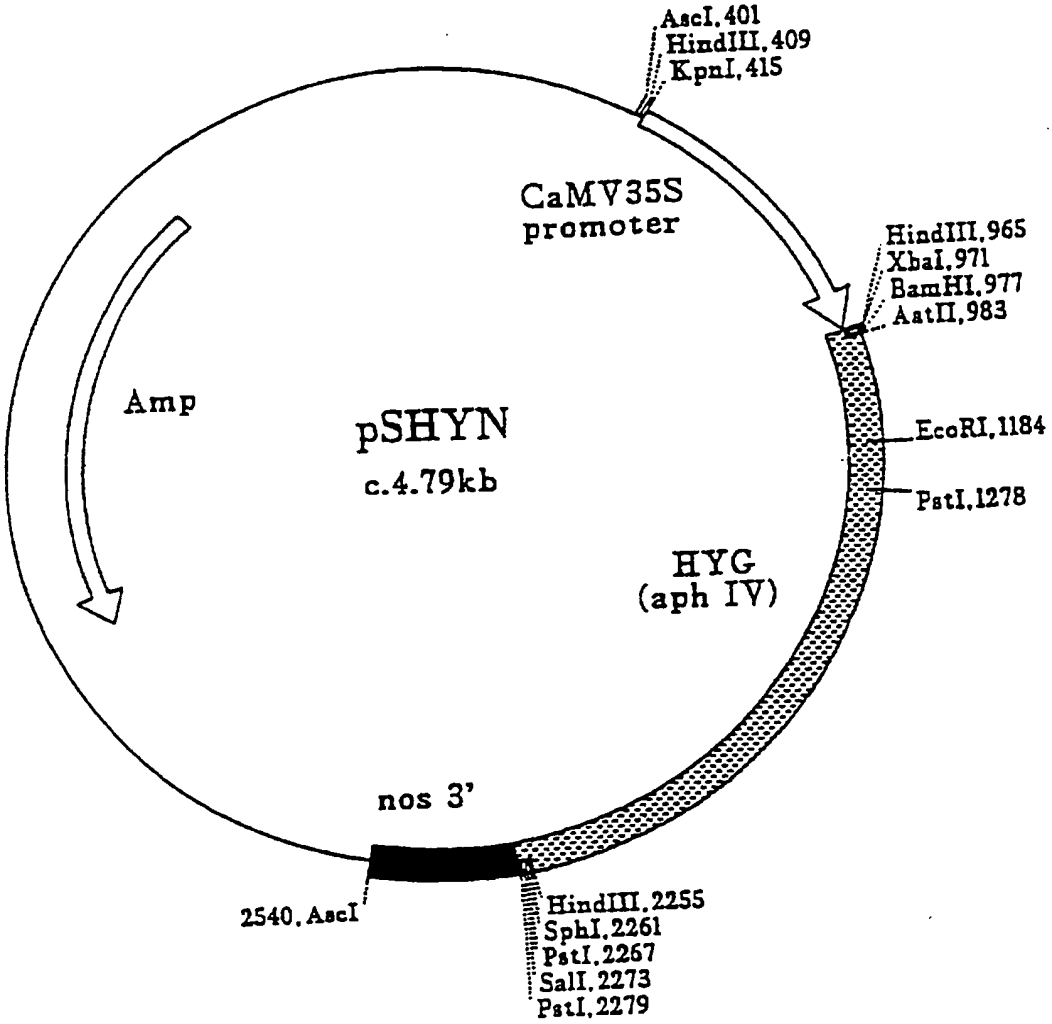
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c.4.79kb
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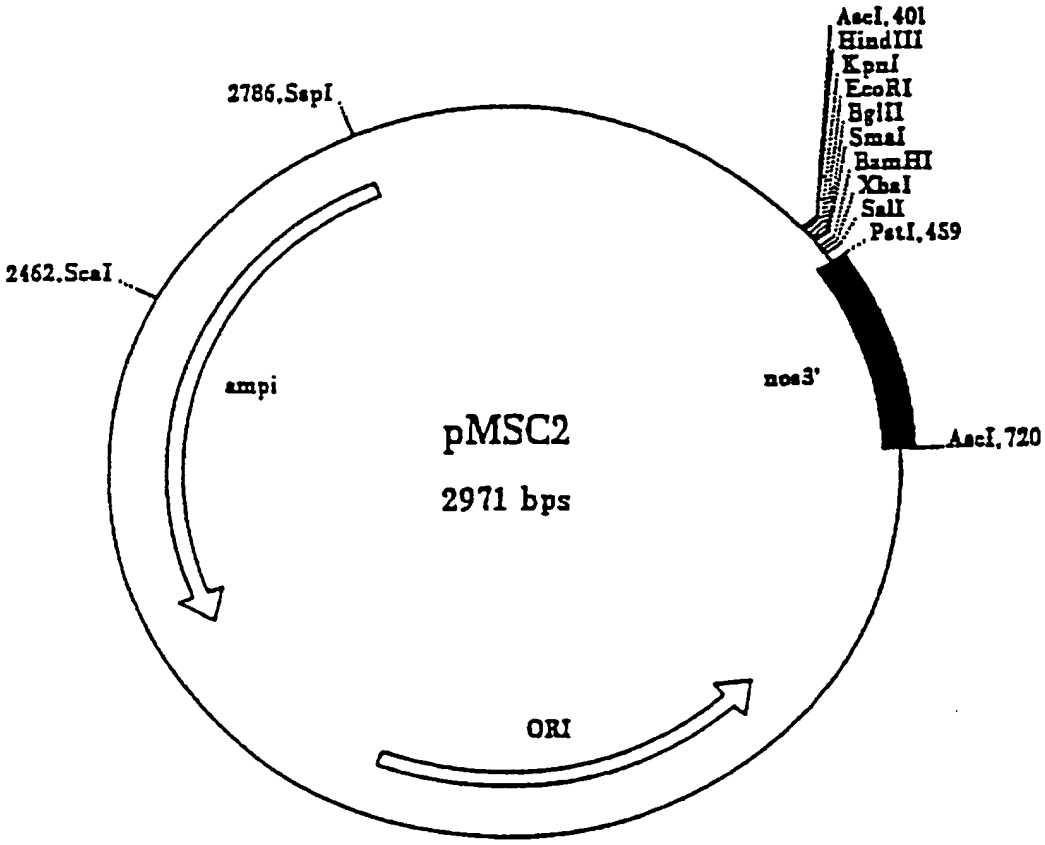
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2462, ScaI
ampi
nos3'
AscI, 720
pMSC2
2971 bps
ORI

BUDAPEST TREATY ON THE INTERNATIONAL
RECOGNITION OF THE DEPOSIT OF MICROORGANISMS
FOR THE PURPOSES OF PATENT PROCEDURE

INTERNATIONAL FORM

Zeneca Limited,
Jealott's Hill Research
Station,
Bracknell,
Berkshire.
RG12 6EY

VIABILITY STATEMENT
issued pursuant to Rule 10.2 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified on the following page

NAME AND ADDRESS OF THE PARTY
TO WHOM THE VIABILITY STATEMENT
IS ISSUED

I. DEPOSITOR	II. IDENTIFICATION OF THE MICROORGANISM
Name: AS ABOVE Address:	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: NCIMB 40814 Date of the deposit or of the transfer: 9 July 1996

III. VIABILITY STATEMENT

The viability of the microorganism identified under II above was tested on 11 July 1996 [2]. On that date, the said microorganism was

[3] [X] viable

[3] [ ] no longer viable

[1] Indicate the date of the original deposit or, where a new deposit or a transfer has been made, the most recent relevant date (date of the new deposit or date of the transfer).

[2] In the cases referred to in Rule 10.2(a)(ii) and (iii), refer to the most recent viability test.

[3] Mark with a cross the applicable box.

IV. CONDITIONS UNDER WHICH THE VIABILITY TEST HAS BEEN PERFORMED[4]

INTERNATIONAL DEPOSITARY AUTHORITY

Name: NCIMB Ltd

Address: 23 St Machar Drive
Aberdeen Scotland
UK

Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s):

Date: 12 July 1996

[4] Fill in if the information has been requested and if the results of the test were negative.

Zeneca Limited,
Jealott's Hill Research
Station,
Bracknell,
Berkshire.
RG12 6EY

BUDAPEST TREATY ON THE INTERNATIONAL
RECOGNITION OF THE DEPOSIT OF MICROORGANISMS
FOR THE PURPOSES OF PATENT PROCEDURE

INTERNATIONAL FORM

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT
issued pursuant to Rule 7.1 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

NAME AND ADDRESS
OF DEPOSITOR

I. IDENTIFICATION OF THE MICROORGANISM

Identification reference given by the DEPOSITOR:	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY:
lambda phage banana cDNA library U2	NCIMB 40814

II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION

The microorganism identified under I above was accompanied by:

[ ] a scientific description

[X] a proposed taxonomic designation

(Mark with a cross where applicable)

III. RECEIPT AND ACCEPTANCE

This International Depositary Authority accepts the microorganism identified under I above, which was received by it on 9 July 1996 (date of the original deposit)[1]

IV. RECEIPT OF REQUEST FOR CONVERSION

The microorganism identified under I above was received by this International Depositary Authority on (date of the original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on (date of receipt of request for conversion)

V. INTERNATIONAL DEPOSITARY AUTHORITY

Name: NCIMB Ltd

Address: 23 St Machar Drive
Aberdeen Scotland
UK AB2 1RY

Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s):

Date: 12 July 1996

1 Where Rule 6.4(d) applies, such date is the date on which the status of international depositary authority was acquired.

Form BP/4 (sole page)